

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: December 1, 2002, 07:36:12 ; Search time 63 Seconds  
(without alignments)

8202.386 Million cell updates/sec

Title: US-09-854-562-1

Perfect score: 1685  
1 CTTAAAAACATTATTATTTC.....TTCCAAAAA.....1685

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 segs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :  
1: /cgn2\_6/prodata/1/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/prodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/prodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/prodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/prodata/1/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/prodata/1/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1685	100.0	1685	1	US-08-362-512A-1
2	1685	100.0	1685	4	US-08-964-939-1
3	507.8	30.1	1740	1	US-08-362-512A-3
4	507.8	30.1	1740	4	US-08-964-939-3
5	53.2	3.2	1882	4	US-09-370-253-1
6	51.6	3.1	1015	4	US-09-370-253-3
7	47.6	2.8	1865	4	US-09-370-253-5
8	46	2.7	1703	4	US-09-370-253-9
9	37.2	2.2	7218	1	US-08-332-463-14
10	36.2	2.1	1960	4	US-09-513-057C-12
11	36.2	2.1	1617	4	US-09-513-057C-14
12	35.4	2.1	1541	4	US-09-149-476-65
13	35.4	2.1	7218	1	US-08-332-463-14
14	35.2	2.1	1863	4	US-09-513-057C-1
15	35	2.1	2088	4	US-09-513-057C-4
16	35	2.1	2518	4	US-09-513-057C-1
17	35	2.1	2606	4	US-09-234-827B-3
18	35	2.1	4221	4	US-09-513-057C-3
19	35	2.1	4221	4	US-09-513-057C-34
20	35	2.1	8302	4	US-09-234-827B-1
21	34.4	2.0	756	3	US-08-822-322-7
22	34.4	2.0	756	4	US-09-466-109-7
23	34.4	2.0	1001	4	US-09-641-638-89
24	34.2	2.0	915	4	US-09-149-476-157
25	34.2	2.0	915	4	US-09-149-476-294
26	34	2.0	1533	4	US-09-134-001C-531
27	34	2.0	2322	1	US-08-618-164-1

28	34	2.0	2649	2	US-08-718-964-1	Sequence 1, Appl1
29	34	2.0	2649	2	US-09-059-964A-1	Sequence 1, Appl1
30	34	2.0	2649	2	US-08-842-341-1	Sequence 1, Appl1
31	34	2.0	5703	4	US-09-280-590A-36	Sequence 36, Appl
32	33.4	2.0	530	4	US-09-134-001C-2354	Sequence 2354, Ap
33	33.4	2.0	405	4	US-09-134-001C-2395	Sequence 2395, Ap
34	33.4	2.0	1732	1	US-08-417-330A-17	Sequence 17, Appl
35	33.2	2.0	731	4	US-09-641-638-87	Sequence 87, Appl
36	33.2	2.0	788	4	US-09-641-638-88	Sequence 88, Appl
37	32.8	1.9	616	2	US-08-630-822A-93	Sequence 93, Appl
38	32.8	1.9	616	2	US-09-005-069-93	Sequence 93, Appl
39	32.8	1.9	616	4	US-09-171-156A-42	Sequence 42, Appl
40	32.8	1.9	1065	4	US-08-765-907A-7	Sequence 7, Appl1
41	32.8	1.9	1080	4	US-09-668-680-9	Sequence 9, Appl1
42	32.8	1.9	2619	4	US-08-983-502-17	Sequence 17, Appl
43	32.8	1.9	2619	5	PCT-US96-10521-17	Sequence 17, Appl
44	32.8	1.9	2887	4	US-08-983-502-14	Sequence 14, Appl
45	32.8	1.9	2887	5	PCT-US96-10521-14	Sequence 14, Appl

#### ALIGNMENTS

RESULT 1  
US-08-362-512A-1  
; Sequence 1, Application US/08362512A  
; Patent No. 5719043  
; GENERAL INFORMATION:  
; APPLICANT: FROMMER, Wolf-Bernd  
; TITLE OF INVENTION: DNA SEQUENCES FOR AN AMINO ACID  
; TITLE OF INVENTION: TRANSPORTER, PLASMIDS, BACTERIA, YEASTS AND PLANTS  
; TITLE OF INVENTION: CONTAINING A TRANSPORTER AND THEIR USE  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ostroienk, Faber, Gerb & Soffen  
; STREET: 1180 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: US  
; ZIP: 10036-8403  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/362,512A  
; FILING DATE: 05-JAN-1995  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/007,636  
; FILING DATE: 21-JAN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meliman, Edward A.  
; REGISTRATION NUMBER: 24,735  
; REFERENCE/DOCKET NUMBER: P/951-107  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 382-0700  
; TELEFAX: (212) 382-0888  
; TELEX: 236925  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1685 base pairs  
; TYPE: nucleic acid  
; STRANDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; ORGANISM: Arabidopsis thaliano  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 57..1511  
; OTHER INFORMATION: /note= "amino acid transporter"





Qy 1691 AAAAA 1685  
Dy 1681 AAAAA 1685

## RESULT 3

US-08-362-512A-3  
: Sequence 3, Application US/08362512A  
: Patent No. 5719043  
: GENERAL INFORMATION:  
: APPLICANT: FROMMER, Wolf-Bernd  
: TITLE OF INVENTION: DNA SEQUENCES FOR AN AMINO ACID  
: TITLE OF INVENTION: TRANSPORTER, PLASMIDS, BACTERIA, YEASTS AND PLANTS  
: TITLE OF INVENTION: CONTAINING A TRANSPORTER AND THEIR USE  
: NUMBER OF SEQUENCES: 4

: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Ostrolenko, Faber, Gerb & Soffen  
: STREET: 1180 Avenue of the Americas  
: CITY: New York  
: STATE: NY

: COUNTRY: US  
: ZIP: 10036-8403  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: Patent in Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/362,512A  
: FILING DATE: 05-JAN-1995  
: CLASSIFICATION: 800

: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 08/007,636  
: FILING DATE: 21-JAN-1993  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Meilman, Edward A.

: REGISTRATION NUMBER: 24,735  
: REFERENCE/DOCKET NUMBER: P/951-107  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (212) 382-0700  
: TELEX: 236925

: INFORMATION FOR SEQ ID NO: 3:

: SEQUENCE CHARACTERISTICS:  
: LENGTH: 1740 base pairs  
: TYPE: nucleic acid  
: STRANDEDNESS: single  
: TOPOLOGY: linear  
: MOLECULE TYPE: cDNA  
: ORIGINAL SOURCE:  
: ORGANISM: Arabidopsis thaliana

: FEATURE:  
: NAME/KEY: CDS  
: LOCATION: 80..1558  
: OTHER INFORMATION: /product= "amino acid transporter"

US-08-362-512A-3

Query Match 30.1%; Score 507.8; DB 1; Length 1740;  
Best Local Similarity 59.2%; Pred. No. 7.8e-154;  
Matches 921; Conservative 0; Mismatches 627; Indels 7; Gaps 3;

Qy 135 AAGAACCTCGATGAGATGGTCGAGAGAGCGTACCGGAGCTGGCTTACCGCGAGTGG 194  
Dy 185 AATGCTTCGATGATGATGCGCCCTCAAGAACTGGGACTGTGTTGACCGCGAGCT 244  
Qy 195 CATATTATCAGCGGCTGATGAGCTCCGAGTGTGTCTTTAGCATGGGCTATAGCTCAG 254  
Dy 245 CATATAATAACTCGGTTATCGGATCCGGGTTTTGTCTATTGGCGTGGCGGATTGCAAC 304  
Qy 255 CTTCGTTGGATCCGAGGACATCGATCTTACTCATTTCTCGTTTCATTACTTACTCACC 314  
Dy 305 CTCGGATGGATCGCTGGCCCTGCTGTGATGCTATTGTTCTCTCTGTGTACTCTTACTCC 364

Qy 315 TCCACCAATGCTTCCCGAATTGCTACCGTGGCGCGGATCCCGTACCGGAAAAACGGAATTAC 374  
Dy 365 TCCACACTTCTTAGCGACTGCTACAGAAACCGCGGATGCAAGTGTCTGCGAAGAGAACTAC 424  
Qy 375 ACTTACATGAGCGTTGTTCCGATCTTACCTCGTGTAGGAAAGTGACGCTCTGTGGAGTG 434  
Dy 425 ACTTACATGAGTCCGTTCCGATCAATTCTCGTGGGTTCAAGTTCAGAGATTGTGGGTTG 484  
Qy 435 GCACATATGGGAATCTGATGGGCTCACTGTGTGTACACCATCACTGTCTTCTATTAGT 494  
Dy 485 ATTCAATCTTGAATCTCTTTGGTATCGCAATTGGATACACGATAGCAGCTTCCATAAGC 544  
Qy 495 TTGTAGCGGTAGGGAATTCGAATGCTTCCACGATAAAGGCGACACTGCGGATTGTACT 554  
Dy 545 ATGATGCGATCAAGAGATCCAACTGCTTCCACAGAGTGGAGAAAGACCCATGTCCAC 604  
Qy 555 ATATGGAATATCCGATATGCGGTTTGTGTATCAATCAAGTTATTCTTAGCCAGATC 614  
Dy 605 ATGTCCAGTAATCTTTACATGATCGTATTTGGTGTGGCAGAGATCTTGTCTCTCAGGTT 664  
Qy 615 CCAAAATTCACAAAGCTCTCTTTCTTTCCATTATGGCGCGAGTCATGTCTTTACTTAT 674  
Dy 665 CTTGATTTGATCAGATTGTTGGATCTCCATTGTTGAGCTGTATGTCTCTTCACTTAC 724  
Qy 675 GCAACTATTGGAAATCGGTTCTAGCCATCGCAACCGTCCGAGTGGGAAAGTGGTAAGACG 734  
Dy 725 TCTGCCATTTGCTAGCTCTTGGAAATCGTTCAAGTTGCGCGAATGGAATTTTCAAAGGA 784  
Qy 735 AGTATGACGGGACAGCGGTTGAGTAGATGTAACCGCAGCTCAAAAGATATGGAGATCG 794  
Dy 785 AGTCTACTTGGATAGCATCGAACA---GTGACTCAACACAGAGAGATATGGAGACC 841  
Qy 795 TTTCAGCGGTTGGGACATAGCGTTTCCGCTATGCTTATGCGCGGTTCTCATCGAGATT 854  
Dy 842 TTCCAAGCACTTGGAGACATTTGCTTTTCGCTACTCATACTCTGTGTCTTAATCGAGATT 901  
Qy 855 CAGGATACACTAAGATCTAGCCAGCTGAGAAACGCGCATGAAAGAGCAAGTCTTTGTG 914  
Dy 902 CAGGATCTGTAAGATCCCAACCGGGGAATCGAAACGATGAAGAAAGCAAAAAATC 961  
Qy 915 GAGATCAACACCACTTTTTCATCATCTTATGTGTGATGCAATCGGCTATGCTGCAATT 974  
Dy 962 AGTATTCGCTCACAACTATCTTACATGCTATGTGGCTCAATGGGTTATGCGGCTTT 1021  
Qy 975 GGAACCAATGCCCTCGAGATTCTCTACAGATTTCGGGTTTTTCGAGCCCTTTTGGCTC 1034  
Dy 1022 GGAGTGCAGCACCGGGAACCTCTCACCGGTTTTGGAATCTACAAACCGTTTGGCTC 1081  
Qy 1035 ATTGACTTTGCAAAACGCTTGGATCGCTGTCCACTTATTTGGTGTCTATCAGGTTTCGG 1094  
Dy 1082 CTTGACATAGCTAAACCGCCCATTTGTTCCACCTCTGTGGAGCTTACCAAGTCTTTGCT 1141  
Qy 1095 CAGCGGATATTCAGGTTTCTGAGAAAAATGCAACAGAAACTATCCAGACAAACAGTTTC 1154  
Dy 1142 CAGCCCATCTTTGCTTTATGAAAAATCAGTCCGAGAGATATCCAGCAATGACTTTC 1201  
Qy 1155 ATCACTCTGATATTCAGTAAACGCTAGC---TTTCCTTGGAAAAATTCACATAGCCTC 1211  
Dy 1202 CTCAGCAAGGAATTTGAAATCAGAAATCCCGGATTTAAGTCTCCTTACAAAGTAAACGTT 1261  
Qy 1212 TTCAAGTTGGTGGAGGACACCTTATGTGTTTATAACCACTGTGTAGCTATGATATTC 1271  
Dy 1262 TTCAAGATGTTTACAGGAGTGGCTTTGTCTTACAAACCCGCTGATATCGATGCTGATG 1321  
Qy 1272 CTTTCTTCAACCGCATCTTAGGCTTATCGGAGCAGCTTCTTCTTGGCTTTTAAACGGTT 1331  
Dy 1322 CCGTTTTTAAACGACGTGGTGGGATCTTAGGGCGTTTAGGGCTTTGAGCGCTTGA 1381  
Qy 1332 TATTTCCCTGTGGAGATGCACATTCGCAAAACCAAGATTAAAGAGTACTCTGCTAGATGG 1391  
Dy 1382 TATTTCCGATGGAGATGTATATTAAGCAGGAGAGGTTGAGAAATGGAGCAGAGATGG 1441



Qy 1155 ATCACTTCTGAATATTCAGTAACAGTACC---TTTCTTTGAAATAATCAACATTAGCCTC 1211  
|||  
Db 1202 CTCAGCAAGAAATTTGAAATCAGAAATCCCGGATTTAAGTCTCCCTTACAAAGTAAAGGTT 1261  
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Qy 1212 TTCAGATTGGTGGAGGACAGCTTATGTGGTTATTAACACCTGTTGTAGCTATCATATTC 1271  
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Db 1262 TTCAGGATGGTTTACAGGATGGCTTTGCTTTACAAACCCGCTGATATCAAGTCTGATG 1321  
|||  
Qy 1272 CTTTCTTCAACCGCATTTAGTCTTATCGGAGCAGCTTCTCTCGGCCCTTTAAACGGTT 1331  
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Db 1332 CCGTTTTTAAACGACGTGGTCGGATCTTAGGGCGTTTAGGCTTTTGGCCCTTGACGGTT 1381  
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Qy 1332 TATTTCCCTGTGGAGTGACATTCGACAAACCAAGATTAGAAGTACTCTGCTAGATGG 1391  
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Db 1382 TATTTCCGGTGGAGATGGTATTTAAGCAGAGAGAGGTTTGAATAATGGAGCAGAGTGG 1441  
|||  
Qy 1392 ATTGCGCTGAAACGATGTGCTATGTTGCTTGTGCTGCTGCTCTTAGCTGCGACCGGA 1451  
|||  
Db 1442 GTGTGTTTACAGATGCTTAGTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGGA 1501  
|||  
Qy 1452 TCCATCGCAGGACTTATAGTACTGTCAAAACCTCAAGCCCTTCGGACTATCATGAG 1511  
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Db 1502 TCAATCCCGGAGTGTGCTTGTATCTTAAGTCTTAAGCCATTAAGTCTACATATGA 1561  
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Qy 1512 TGAGTTTGAGATCCTCAAGAGAGTCAAAATATATGTAGTGTGCTTTCTGTTTAA 1571  
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Db 1562 TGATTTGGACCATGAACAAACAGAGAGTGTGCTGTGAAGTTTACCATTTCAAAGAAA 1621  
|||  
Qy 1572 CTATCTGGTCTAAATCCAATCAG-AATGCTTTATGCTAAATTCATGAATCTCTCT 1630  
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Db 1622 ACTCCAAAATGTATATTGTATGTTGTTCTCAATTCGTATGGTCTCATCTTTGTATTA 1681  
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Qy 1631 GTATCTACATCTTCAATCTAATACATATGAGCTCTTCCAAAATAAAAAAAAAAAAA 1685  
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Db 1682 AAATTTAAACTTATGTTATAAATATATAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1736  
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## RESULT 5

US-09-370-253-1  
; Sequence 1, Application US/09370253  
; Patent No. 6165792  
; GENERAL INFORMATION:  
; APPLICANT: Allen, Stephen M.  
; APPLICANT: Sakai, Hajime  
; APPLICANT: Thorpe, Catherine J.  
; TITLE OF INVENTION: Amino Acid Transporters  
; FILE REFERENCE: BB-1200  
; CURRENT APPLICATION NUMBER: US/09/370,253  
; EARLIER FILING DATE: 1999-08-09  
; EARLIER FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 1  
; LENGTH: 1882  
; TYPE: DNA  
; ORGANISM: Hordeum vulgare  
US-09-370-253-1

Query Match 3.2%; Score 53.2; DB 4; Length 1882;  
Best Local Similarity 51.1%; Pred. No. 9, 5e-07;  
Matches 183; Conservative 0; Mismatches 163; Indels 12; Gaps 2;

Qy 768 ACCGACGCTCAAAAGATATGGAGATCGTTTCAAGCGGTTGGGGACATAGCGCTTAC 827  
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Db 730 ACGACAGCGGCGAGGTTGTTGTTTCTTTGGGGGGCTCGGCGATGTGGCATTTCTCCTAC 789  
|||  
Qy 828 GCTTATGCCACGGTTCTCATCGAGATTCAAGATACACTAAGATCTAGCCACAG-----CT 881  
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Db 790 TCCGGCCACAATGTGGTCTAGAAATTCAGGCTACCATCCCATCGACGCCGGCAACCG 849  
|||  
Qy 882 GAGAAACGCAATGAAAGAGCAAGTCTTTGTGGGAGTATCAACCAACCATCTTTTCTAC 941  
|||

Db 850 TCCAAAGACCAATGTGGAGGGCGTGGTGGCCCTACATCATCATCGCCGCTGCTAC 909  
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Qy 942 ATCTTATGTGATGATCGGCTATGCTCATTTTGGAAACAATGCCCTCGAGATTTCTCTC 1001  
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Db 910 TTCCCGGTGCAATTTATCGGCTACTGGGCAATTTGGCAACAGCGTCGAGACAACATCCTC 969  
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Qy 1002 ACAGATTTGGGTTTTTCAGGCCCTTTTGGCTCATTTGCAATGCTTGCATGCT 1061  
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Db 970 A-----TCACCCCTCAACAGCCCAAGTGGCTCATGCCCATGGCCAAACATGATGGTCGTC 1023  
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Qy 1062 GTCCACCTTATTTGGTGCCTTATCAGGTGTTCCGCGAGCGCATATTCACAGTTTGTGAGA 1119  
|||  
Db 1024 GTTCACTCATCGTAGCTACCAAGATTTATGGATGCCGTTTGTGACATGATGAGA 1081  
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## RESULT 6

US-09-370-253-3  
; Sequence 3, Application US/09370253  
; Patent No. 6165792  
; GENERAL INFORMATION:  
; APPLICANT: Allen, Stephen M.  
; APPLICANT: Sakai, Hajime  
; APPLICANT: Thorpe, Catherine J.  
; TITLE OF INVENTION: Amino Acid Transporters  
; FILE REFERENCE: BB-1200  
; CURRENT APPLICATION NUMBER: US/09/370,253  
; EARLIER FILING DATE: 1999-08-09  
; EARLIER FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 3  
; LENGTH: 1016  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-09-370-253-3

Query Match 3.1%; Score 51.6; DB 4; Length 1016;  
Best Local Similarity 50.8%; Pred. No. 2, 1e-06;  
Matches 182; Conservative 0; Mismatches 164; Indels 12; Gaps 2;

Qy 768 ACCGACGCTCAAAAGATATGGAGATCGTTTCAAGCGGTTGGGGACATAGCGTTTCGCTAT 827  
|||  
Db 98 ACCACGCGCGGGAAGGTGTTTCGGCTTCTTCGGCGCGCTGGGGAGCTGGCGTTTCGCTAC 157  
|||  
Qy 828 GCTTATGCCACGGTTCTCATCGAGATTCAGATACACTAAGATCTAGCCAGCTGAG--- 884  
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Db 158 GCGGCCACACACGTGGTGTCTGGAGATCCAGGCCACCATCCCGTCCACCCCGAAGACCG 217  
|||  
Qy 885 ---AACAAAGCCATGAAAGAGCAAGTCTTTGTGGAGTATCAACACCACTTTTTTCTAC 941  
|||  
Db 218 TCCAAGAAAGCCCATGTTGGAAAGGCGTGTGCTCGCTAGCTGCTGGTGGGCTCTGCTAC 277  
|||  
Qy 942 ATCTTATGTGATGATCGGCTATGCTCATTTGGAACAATGCCCTCGAGATTTCTCTC 1001  
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Db 278 TTCCCGCTCGGCTCATCGGCTACTTGGGCGGTTTCGGAACAACAGGTCGAGGACAACATCCTC 337  
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Qy 1002 ACAGATTTGGGTTTTTCGAGGCCCTTTTGGGCTCATTTGACATTTTGCMAACGCTTGCATCGCT 1061  
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Db 338 A-----TCACGCTCAGCAAGCCCAAGTGGCTCATCGGCTCGCCAAACATGATGGTCGTC 391  
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Qy 1062 GTCCACCTTATTTGGTGCCTTATCAGGTGTTCCGCGACGCGATATTCAGTATTTGTGAGA 1119  
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Db 392 GTCCATGTCATCGGACGCTACCAAGATCTATGCCATGCCGTTTGTGACATGATGAGA 449  
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## RESULT 7

US-09-370-253-5  
; Sequence 5, Application US/09370253  
; Patent No. 6165792  
; GENERAL INFORMATION:  
; APPLICANT: Allen, Stephen M.







Db 2775 C 2775

RESULT 12  
US-09-149-476-65  
Sequence 65, Application US/09149476  
Patent No. 6420526  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: 186 Human Secreted proteins  
FILE REFERENCE: P2002P1  
CURRENT APPLICATION NUMBER: US/09/149,476  
EARLIER FILING DATE: 1998-09-08  
EARLIER APPLICATION NUMBER: PCT/US98/04493  
EARLIER FILING DATE: 1998-03-06  
EARLIER APPLICATION NUMBER: 60/040,162  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,333  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/038,621  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,626  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,334  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,336  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,163  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/047,600  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,615  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,597  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,502  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,633  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,583  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,617  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,618  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,503  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,592  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,581  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,564  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,500  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,587  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,492  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,598  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,613  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,582  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,596  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,612  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,632  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,601  
EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/043,580  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,568  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,314  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,569  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,311  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,671  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,674  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,669  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,312  
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EARLIER APPLICATION NUMBER: 60/043,672  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,315  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/048,974  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/056,886  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,877  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,889  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,893  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,630  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,878  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,662  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,872  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,882  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,637  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,903  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,888  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,879  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,880  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,894  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,911  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,636  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,874  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,910  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,864  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,631  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,845  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,892  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057,761



Oy 884 GAACAAGCCATGAAAGACAGTCTGTGGAG 918  
Db 1258 RRRRRRRRRRRRRRRRRRRRRRRRRRR 1224

RESULT 14  
US-09-637-118B-1  
; Sequence 1, Application US/09637118B  
; Patent No. 6423838  
; GENERAL INFORMATION:  
; APPLICANT: Hitachi LTD  
; TITLE OF INVENTION: A gene for proline transporter in rice  
; FILE REFERENCE: NITT.0008:NT0114US  
; CURRENT APPLICATION NUMBER: US/09/637,118B  
; CURRENT FILING DATE: 2000-08-11  
; PRIOR APPLICATION NUMBER: JP 230291  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 1863  
; TYPE: DNA  
; ORGANISM: Oryza sativa L.  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 144..1562  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: AB022783  
; DATABASE ENTRY DATE: 1999-01-25  
US-09-637-118B-1

Query Match 2.1%; Score 35.2; DB 4; Length 1863;  
Best Local Similarity 49.5%; Pred. No. 0.63;  
Matches 91; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

Oy 1196 ATTCACATTAGCTCTTCAGATTGCTGGAGACAGCTTATGTGTTATTAACCACTGT 1255  
Db 1253 AATCCACACATATATGTCAGAGTGGGTGTCAAGAGAGGCTACCTGACCGTCACACCTT 1312  
Oy 1256 TGTAGCTATGATATTCCTTCCTTCAACGCGATCTTAGGTCCTATCGAGAGCTTCCTT 1315  
Db 1313 GTGGCCGCCGATGCTCCCTTCCTTGGCGACTTCATGAGCTGACGGGTGACCTCAGAC 1372  
Oy 1316 CTGGCCTTTAAGGTTATTTCCCTGTGAGATGACATTTGCAAAACCAAGATTAGAA 1375  
Db 1373 CTTTCCCTGACATTCCTTGTGAATCACATGTACTCAGGTGAAGCAGAACAGAT 1432  
Oy 1376 GTAC 1379  
Db 1433 GTCC 1436

RESULT 15  
US-09-513-057C-4  
; Sequence 4, Application US/09513057C  
; Patent No. 6433251  
; GENERAL INFORMATION:  
; APPLICANT: Wagner, et al.  
; TITLE OF INVENTION: GENES REGULATING CIRCADIAN CLOCK FUNCTION AND PHOTOPERIODISM  
; FILE REFERENCE: 1505-54357  
; CURRENT APPLICATION NUMBER: US/09/513,057C  
; CURRENT FILING DATE: 2000-02-24  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 2088  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-513-057C-4

Query Match 2.1%; Score 35; DB 4; Length 2088;  
Best Local Similarity 55.3%; Pred. No. 0.79;  
Matches 68; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

Oy 1066 ACCTTATTTGGTGCCTATCAGTCTTCGCCAGCCGATATTCAGTTTGTGAAATAAT 1125  
Db 1076 AACTTATTTGCTGCATCAGCGATCTTCTCTGATGAGATCAGTTTCTTGAAAAAGTTT 1135  
Oy 1126 GCAACAGAACTATTCAGACACACAGTTCATCTTGAATATTCAGTAAACGTA 1185  
Db 1136 CTGCTAAAGCTATCCAGTGAAGAAAGCTCTTCATCAGAAATTTCTGTTAAAGCCTC 1195  
Oy 1186 TCC 1188  
Db 1196 TAC 1198

Search completed: December 1, 2002, 09:04:31  
Job time : 95 secs



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: December 1, 2002, 08:21:37 ; Search time 3116 Seconds  
(without alignments)  
15737.557 Million cell updates/sec

Title: US-09-854-562-1

Perfect score: 1685  
Sequence: 1 CTTAAACATTATTATTATC.....TTCGAAAAAAAAAAAAA 1685

Scoring table: IDENTITY NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
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2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_ov:\*  
5: gb\_ov:\*  
6: gb\_ov:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
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11: gb\_ro:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
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22: em\_ov:\*  
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28: em\_un:\*  
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37: em\_htg\_mam:\*  
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40: em\_htgo\_hum:\*  
41: em\_htgo\_mus:\*  
42: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1685	100.0	1685	A37879	A37879 Sequence 1
2	1685	100.0	1685	A95148	A95148 Sequence 1
3	1685	100.0	1685	AR157916	AR157916 Sequence 1
4	1685	100.0	1685	188787	188787 Sequence 1
5	1685	100.0	1685	ATPPMR	X67124 A.thaliana
6	1646	97.7	1665	ATPPMR	L16240 Arabidopsis
7	1593.6	94.6	1644	ATPPMR	AY069889 Arabidops
8	723.4	42.9	1658	ATPPMR	X5726 A.thaliana
9	722.2	42.9	77636	AB077822	AB077822 Arabidops
10	722.2	42.9	66014	FI9C14	AC008051 Sequence
11	721.2	42.8	5798	AF031649	AF031649 Arabidops
12	558.8	33.2	1157	STAP1	Y09825 S.tuberosum
13	556.8	33.0	1500	RCO7574	AU007574 Ricinus C
14	552	32.8	1136	AF080542	AF080542 Nepenthes
15	518.6	30.8	1619	ATLBAAP4	X77500 Arabidopsis
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19	507.8	30.1	1740	A37880	A37880 Sequence 2
20	507.8	30.1	1740	A95149	A95149 Sequence 2
21	507.8	30.1	1740	AR157917	AR157917 Sequence 3
22	507.8	30.1	1740	188788	188788 Sequence 3
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26	507.2	30.1	1794	AY085581	AY085581 Arabidops
27	507.2	30.1	1867	ATLBAAP3	X77459 Arabidopsis
28	504.8	30.0	1761	AY090341	AY090341 Arabidops
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30	490.2	29.1	1127	STAP2	Y09826 S.tuberosum
31	480.2	28.5	1879	VFAACMTRA	Y09591 V.faba mRNA
32	478.4	28.4	1832	ATLBAAP5	X77501 Arabidopsis
33	469.8	27.9	1450	VFA318811	A3318811 Victoria fab
34	454.6	27.0	1580	VFA318809	A3318809 Victoria fab
35	438.2	26.0	852	RCAACAR	Y11121 Ricinus com
36	432.2	25.6	1110	AF080543	AF080543 Nepenthes
37	413.6	24.5	1129	AF080544	AF080544 Nepenthes
38	376.8	22.4	789	AF061434	AF061434 Victoria fab
39	375.8	22.3	1878	VFA318810	A3318810 Victoria fab
40	366.2	21.7	852	RCAACMR	Z68759 R.communis
41	364	21.6	121322	CNS07YBY	AU713953 Oryza sat
42	353.6	21.0	1500	AY052209	AY052209 Arabidops
43	351	20.8	139043	AC090974	AC090974 Oryza sat
44	351	20.8	168033	AP003405	AP003405 Oryza sat
45	351	20.8	183580	AP003561	AP003561 Oryza sat

# ALIGNMENTS

RESULT 1  
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LOCUS A37879  
DEFINITION Sequence 1 from Patent WO9401559.  
ACCESSION A37879  
VERSION A37879.1 GI:2294549  
KEYWORDS  
SOURCE Arabidopsis thaliana.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliopsida; euclcotyledons; core euclcot;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
REFERENCE  
AUTHORS Frommer W.  
TITLE DNA SEQUENCES FOR AN AMINO ACID TRANSPORTER, PLASMIDS, BACTERIA,













QY	1561	TTTCTGTTAAACATCTCGTGTGCTTAAATCCACATGGAATGCTTATTGCTTAAACTTCAT	1620
QY	1621	GAATCTCTGCTGATCTACATCTTTCAATCTATATACATATGAGCTTTCCAAAAA	1680
DB	1621	GAATCTCTGCTGATCTACATCTTTCAATCTATATGAGCTTTCCAAAAA	1680
QY	1681	AAAAA 1685	
DB	1681	AAAAA 1685	
RESULT 6			
ATHAAT		ATHAAT	1665 bp mRNA linear PLN 30-SEP-1993
LOCUS		Arabidopsis thaliana amino acid transporter mRNA, complete cds.	
DEFINITION		116240.1 GI:404018	
ACCESSION		116240	
KEYWORDS		amino acid transporter.	
SOURCE		Arabidopsis thaliana	
ORGANISM		Arabidopsis thaliana cDNA to mRNA.	
REFERENCE		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	
AUTHORS		1 (bases 1 to 1665)	
TITLE		Hsu, L.C., Chiu, T.J., Chen, L. and Bush, D. R.	
JOURNAL		Cloning a plant amino acid transporter by functional complementation of a yeast amino acid transport mutant	
MEDLINE		Proc. Natl. Acad. Sci. U.S.A. 90 (16), 7441-7445 (1993)	
PUBMED		93361464	
FEATURES		8356039	
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		/protein_id="AAA2726.1"	
		/db_xref="GI:404019"	
		/translation="MKSFTEGHNHSTAESGDAVTVSDPTKNVDEGKERTGWTMLTA	
		SAHITAVIGSGVLSLMAVILKGLMIGTSLILFFPIYFTSMALACVAPAPVVGIG	
		KENYIMVVRVSYGKRGVQLCGVAQGNLIGVTGYTTAISLVAAGKNCDFDKG	
		HRADDTISNYPVMAVFGIIOVILSOIPNPKFSPLSIMAASFPYRTIGLALATY	
		AGKRGKSMGTAVGVNDVPAKQITKMSPKAVNDIAPAYATVYLIEIDTLRSSPAP	
		NKAMRASLVGSVSTTFPIYILGGIGYAAAGNAPEDPIYDGFEPFPLIDFAAC	
		AVHILGAVQVFRQPIFOFVEKKCRNRPDKRFTTSYSVNVFLEKFNISLPIVMRT	
		AAVTVIVVMVIFPENALIDELIGAAASFVPLIYFVEVNHIAQTKIKYSAFWIALKTK	
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Best Local Similarity	99.4%;	Pred. No.0;	
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QY	1	CTTAAACATTTATTTATCTCTCTCTGTTCTCTCTTTCTCTTTCTCTGATGACTATGA	60
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QY	61	AGAGTTCAACAGAAAGACACACACATCCACGCGGAGATCCGGGATGCGCTACACCG	120
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QY	121	TGTGCGACCCGACAAAGAACGTCGATGAAGATGTCGAGAGAACGTAACCGGACGTCGC	180
DB	121	TGTGCGACCCGACAAAGAACGTCGATGAAGATGTCGAGAGAACGTAACCGGACGTCGC	180
QY	181	TTACGCGAGATGCGCATATATATACGCGCGGTATAGGCTCCGGAAGTGTCCTTTAGCAT	240
DB	181	TTACGCGAGATGCGCATATATATACGCGCGGTATAGGCTCCGGAAGTGTCCTTTAGCAT	240
QY	241	GAGGCTAATGCTACGCTTGTTGGTGAATGCGAGGACATGCATCTTAATCTTCCTGTTCA	300

Db	241	GGGCTATAGCTACACTTGGTGGATGCGAGGACATCGATCTTACGATTTTCTGCTTCA	300
Qy	301	TTACTTACTTCACTCCACCACTGCTTGCCGATTTGCTACCGTGGCCGGATCCCGTCA	360
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Qy	361	GAAGAACGAATTACATTACATGAGACGCTGTGTCATCTTACCTCGTGGTAGAAGATGC	420
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Qy	541	CTGGCGATTGATCTATATGCAATATACGGTATATGGGGGTTTTGGTATCATTTCAAGTTA	600
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Qy	601	TTCTTAGCCAGATCCCAAAATTTCCAAAGCTCTCTTTCTTTCATTTATGGCCGACATCA	660
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Qy	661	TGTCCTTACTTATAGCAACTATTTGGAAATGGCTTAGCCATATGCAACCGTCGAGGTGGGA	720
Db	661	TGTCCTTACTTATAGCAACTATTTGGAAATGGCTTAGCCATATGCAACCGTCGAGGTGGGA	720
Qy	721	AAGTGGGTAAAGCAGATATGACGGGACACGCGTTGGAGTAGATGTTAACCGCACTCAAA	780
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Qy	901	GAGCAAGCTGTGGAGATGTCAACACACACTTTTCTCATCTTATATGAGATGCATCG	960
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Qy	961	GCTATGCTGCATTTGGAAACAATGCCCCCTGAGATTTCTTCACAGATTTCCGGATTTTTCG	1020
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Qy	1021	AGCCCTTTGGCTATTTGATCTTGGCAAAAGCTTGATGCTGTCCACTTTATTTGGTGCT	1080
Db	1021	AGCCCTTTGGCTATTTGATCTTGGCAAAAGCTTGATGCTGTCCACTTTATTTGGTGCT	1080
Qy	1081	ATCAGGTGTTGGCGACGCGATATTCACAGTTGTTGAGAAAAAATGCAACAGAAATCTATC	1140
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Qy	1141	CAGACAAAGTCAATCACTTCTGAAATATTCAGTAAAGATGATCCCTTCTTGGAAATTTCA	1200
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Qy	1201	ACATTAGCCTCTTCAGATGCTGTGAGAGACAGCTTATGTGTGTTATACCACTGTTGTAG	1260
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 QY 1020 GAGCCCTTTGGCTCATGACTTTGCAAGCTTGATCGCTGCTCACTTATGAGTCC 1079  
 DB 1052 GAGCCCTTTGGCTCATGACTTTGCAAGCTTGATCGCTGCTCACTTATGAGTCC 1111  
 QY 1080 TATCAGGCTTTCGCGAGCCGATATTCAGATTTGTTGAGAAAAAATGCAACAGAACTAT 1139  
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 QY 1320 CCTTAAACGGTTTATTTCCCTGAGAGATGACATTTGCACAAAACCAAGATTAGAAGTAC 1379  
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 QY 1380 TCTGCTGAGATGAGTGGCGCTGAGAAAGATGCTATGCTTATGCTTCTCTGCTTA 1439  
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 QY 1440 GCTGACACCGGATTCATCGCAGAGACTTATAGTATGCTCAAAACCTACAGCCCTTCGG 1499  
 DB 1472 GCTGACACCGGATTCATCGCAGAGACTTATAGTATGCTCAAAACCTACAGCCCTTCGG 1531  
 QY 1500 ACTATGATGATGAGTATGATGATCTTCAAGAGAGTCAAAAATATATGATGATTTGCT 1559  
 DB 1532 ACTATGATGATGAGTATGATGATCTTCAAGAGAGTCAAAAATATATGATGATTTGCT 1591  
 QY 1560 CTTTCTGTTAAACTATCTGCTGCTTAATTCATGAGATGCTTATTTGCTA 1611  
 DB 1592 CTTTCTGTTAAACTATCTGCTGCTTAATTCATGAGATGCTTATTTGCTA 1643  
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 LOCUS 1658 bp mRNA linear PLN 08-JAN-1997  
 DEFINITION A.thaliana mRNA for amino acid permease 6.  
 ACCESSION X95736  
 VERSION X95736.1 GI:1769886  
 KEYWORDS AAP6 gene; amino acid permease.  
 SOURCE thale cress;  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 REFERENCE 1 (bases 1 to 1658)  
 AUTHORS Rentsch D., Hirner B., Schmelzer E. and Frommer W.B.  
 TITLE Salt stress-induced proline transporters and salt stress-repressed

broad specificity amino acid permeases identified by suppression of  
 a yeast amino acid permease-targeting mutant  
 Plant Cell 8 (8), 1437-1446 (1996)  
 JOURNAL 86373203  
 MEDLINE 8776504  
 PUBMED 2 (bases 1 to 1658)  
 REFERENCE Rentsch, D.  
 AUTHORS Direct Submission  
 TITLE Submitted (16-FEB-1996) D. Rentsch, Institut fuer Genbiologische  
 JOURNAL Forschung, Inhestr. 63, D-14195 Berlin, FRG  
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TITLE	JOURNAL	Kato,A., Suzuki,M., Kuwahara,A., Ooe,H., Higano-Inaba,K. and Kameda,Y.
MEDLINE	REFERENCE	Isolation and analysis of cDNA within a 300 kb Arabidopsis thaliana genomic region located around the 100 map unit of chromosome 1 Gene 239 (2), 309-316 (1999)
AUTHORS	TITLE	2 Suzuki,M., Kato,A. and Kameda,Y. An RNA-binding protein, AtRBP1, is expressed in actively proliferative regions in Arabidopsis thaliana Plant Cell Physiol. 41 (3), 282-288 (2000)
JOURNAL	MEDLINE	20263341
AUTHORS	TITLE	3 Kato,A. and Kameda,Y. Long repeat sequence within a genomic region located around the 100 map unit of chromosome 1 in Arabidopsis thaliana Unpublished
JOURNAL	REFERENCE	4 Suzuki,M., Kato,A., Nagata,N. and Kameda,Y. An xylanase, AtXyl1, is predominantly expressed in vascular bundles, and four putative xylanase genes were identified in the Arabidopsis thaliana genome Unpublished
REFERENCE	AUTHORS	5 (bases 1 to 77636) Kato,A. and Kameda,Y. Direct Submission
TITLE	JOURNAL	Submitted (11-JAN-2002) Atsushi Kato, Graduate School of Science, Hokkaido University, Division of Biological Sciences; Kita10, West8, Sapporo Kita-ku, Hokkaido 060-0810, Japan (E-mail:atsushiesci.hokudai.ac.jp, Tel:81-11-706-2740, Fax:81-11-706-4851)
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RESULT 11
LOCUS AF031649 5798 bp DNA linear PLN 26-MAR-2002
DEFINITION Arabidopsis thaliana neutral amino acid transport system II (NAT2)
gene, complete cds.
ACCESSION AF031649
VERSION AF031649.1 GI:2654018
KEYWORDS
SOURCE
ORGANISM Arabidopsis thaliana.
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 5798)
Heu, L.C.; Chioi, I.J.; Chen, L. and Bush, D.R.
Cloning a plant amino acid transporter by functional
complementation of a yeast amino acid transport mutant
Proc. Natl. Acad. Sci. U.S.A. 90 (16), 7441-7445 (1993)
93361464
PUBMED 8356039
REFERENCE 2 (bases 1 to 5798)
Chang, H.-C. and Bush, D.R.
Genomic Sequence of NAT2/AAP1 of Arabidopsis
Unpublished
REFERENCE 3 (bases 1 to 5798)
Chang, H.-C. and Bush, D.R.
Direct Submission
Submitted (28-OCT-1997) Plant Biology, University of Illinois at
Urbana-Champaign, 190 ERML, 1201 W. Gregory Dr., Urbana, IL 61801,
USA
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Best Local Similarity 90.0%; Pred. No. 3.9e-188;
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## RESULT 12

LOCUS STAB1 1157 bp mRNA linear PLN 17-DEC-1996  
DEFINITION S.tuberosum mRNA for amino acid transporter AAP1, partial.  
ACCESSION Y09825  
VERSION Y09825.1 GI:1743409  
KEYWORDS AAP1 gene; amino acid transporter; transmembrane protein.  
SOURCE Solanum tuberosum.  
ORGANISM Solanum tuberosum.

REFERENCE 1 (bases 1 to 1157)  
AUTHORS Kwart, M., Laubner, M., Heinke, D., Rentsch, D. and Frommer, W.B.  
TITLE An increased C/N ratio in potato tubers due to antisense inhibition of the leaf H<sup>+</sup>/amino acid transporter STAB1  
Unpublished

## JOURNAL

REFERENCE 2 (bases 1 to 1157)  
AUTHORS Kwart, M.  
JOURNAL Direct Submission  
Submitted (26-NOV-1996) M. Kwart, Max-Planck-Institut fuer Molekulare Pflanzenphysiologie, Karl-Liebknecht-Str. 25, Haus 20, D-14476 Golm, FRG

## FEATURES

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RESULT 13
RCO7574 RCO7574 1500 bp mRNA linear PLN 24-NOV-1998
LOCUS Ricinus communis mRNA for amino acid carrier.
DEFINITION
ACCESSION AJ007574
VERSION AJ007574.1 GI:3293030
KEYWORDS AAP1 gene; amino acid carrier.
SOURCE Ricinus communis.
ORGANISM Ricinus communis.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Malpighiales; Euphorbiaceae; Ricinus.
1 (bases 1 to 1500)
Neelam,A.
Direct Submission
Submitted (01-JUL-1998) Neelam A., University of Leeds, Centre for
Plant Biochemistry and Biotechnology, Leeds, LS2 9JT, UNITED
KINGDOM
2 (bases 1 to 1500)
Marvier,A.C., Neelam,A., Bick,J.A., Hall,J.L. and Williams,L.E.
Cloning of a cDNA coding for an amino acid carrier from Ricinus
communis (RCAAP1) by functional complementation in yeast: kinetic
analysis, inhibitor sensitivity and substrate specificity
Biochim. Biophys. Acta 1373 (2), 321-331 (1998)
98405925
MEDLINE
PUBMED
9733991
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 Caryophyllales; Nephentaceae; Nephentes.  
 REFERENCE 1 (bases 1 to 1136)  
 AUTHORS Schulze, W., Frommer, W.B. and Ward, J.M.  
 TITLE Transporters for ammonium, amino acids and peptides are expressed  
 in pitchers of the carnivorous plant Nephentes  
 JOURNAL Plant J. 17 (6), 101-110 (1999)  
 REFERENCE 2 (bases 1 to 1136)  
 AUTHORS Schulze, W., Frommer, W.B. and Ward, J.M.  
 TITLE Direct Submission  
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 Auf der Morgenstelle 1, Tuebingen 72076, Germany  
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VERSION X77500.1 GI:608670  
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REFERENCE 1 (bases 1 to 1619)  
Fischer W.N.  
AUTHORS Direct Submission  
TITLE Submitted (02-DEC-1998) W.N. Fischer, IGF, Institut f.  
JOURNAL Genbiologische Forschung, Jmhestr. 53, 14195, Berlin, FRG  
REFERENCE 2 (bases 1 to 1619)  
Fischer W.N., Kwart M., Hummel S. and Frommer W.B.  
AUTHORS Substrate specificity and expression profile of amino acid  
TITLE transporters (AAPs) in Arabidopsis  
J. Biol. Chem. 270 (27), 16315-16320 (1995)  
MEDLINE 95332342  
PUBMED 7608199  
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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

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Searched: 2185239 segs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

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## SUMMARIES

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5	501.6	29.8	1759	21	AAO36303
6	445.4	26.4	1375	21	AAO41523
7	362.8	21.5	1404	21	AAO48418
8	191.6	11.4	660	24	ABO65898
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19	41	2.4	1656	22	AAO77208	CDNA encoding sunf
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22	39.2	2.3	7321	24	ABO61337	Signal transductio
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24	39	2.3	6081	24	ABO80193	Human immune syste
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36	36.6	2.2	2644	23	ABO09867	Drosophila melanog
37	36.6	2.2	6096	23	ABO09866	Human ovarian and
38	36.6	2.2	6708	22	ABO07966	Human reproductive
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41	36.2	2.1	1232	21	AAO26455	Human secreted pro
42	36	2.1	1286	21	AAO26455	Human secreted pro
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DR	P-PSDB; AAR47812.



KW Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway;  
XX metabolic pathway; promoter; termination sequence; ss.  
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PF 25-FEB-1999; 99US-0121825.  
XX 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
PR 25-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129845.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130449.  
PR 23-APR-1999; 99US-0130510.  
PR 23-APR-1999; 99US-0130891.  
PR 26-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.  
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PR 04-MAY-1999; 99US-0132484.  
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PR 07-MAY-1999; 99US-0132863.  
PR 11-MAY-1999; 99US-0134256.  
PR 14-MAY-1999; 99US-0134218.  
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PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
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PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
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PR 08-JUN-1999; 99US-0138094.  
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PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139492.  
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PR 18-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
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PR 23-JUN-1999; 99US-0140353.  
  
PR 23-JUN-1999; 99US-0140354.  
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PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
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PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
PR 22-JUL-1999; 99US-0145088.  
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PR 22-JUL-1999; 99US-0145192.  
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PR 23-JUL-1999; 99US-0145224.  
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PR 03-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
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PR 11-AUG-1999; 99US-0148319.  
PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
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PR 17-AUG-1999; 99US-0149175.  
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PR 23-AUG-1999; 99US-0149930.  
PR 23-AUG-1999; 99US-0149930.  
PR 23-AUG-1999; 99US-0149930.  
PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151066.  
PR 30-AUG-1999; 99US-0151080.  
PR 31-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.





PR	04-AUG-1999;	99US-0147204.	Query Match	30.8%;	Score 518.6;	DB 21;	Length 1839;
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PR	06-AUG-1999;	99US-0147303.					
PR	06-AUG-1999;	99US-0147416.					
PR	09-AUG-1999;	99US-0147493.					
PR	09-AUG-1999;	99US-0147935.					
PR	10-AUG-1999;	99US-0148171.					
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PR	12-AUG-1999;	99US-0148341.					
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PR	13-AUG-1999;	99US-0148684.					
PR	13-AUG-1999;	99US-0149368.					
PR	15-AUG-1999;	99US-0149175.					
PR	17-AUG-1999;	99US-0149426.					
PR	18-AUG-1999;	99US-0149722.					
PR	20-AUG-1999;	99US-0149723.					
PR	20-AUG-1999;	99US-0149929.					
PR	23-AUG-1999;	99US-0149902.					
PR	23-AUG-1999;	99US-0149930.					
PR	25-AUG-1999;	99US-0150566.					
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PR	10-SEP-1999;	99US-0153070.					
PR	13-SEP-1999;	99US-0153758.					
PR	13-SEP-1999;	99US-0154018.					
PR	15-SEP-1999;	99US-0154039.					
PR	16-SEP-1999;	99US-0154039.					
PR	20-SEP-1999;	99US-0154779.					
PR	22-SEP-1999;	99US-0155139.					
PR	23-SEP-1999;	99US-0155486.					
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PR	28-SEP-1999;	99US-0156458.					
PR	29-SEP-1999;	99US-0156596.					
PR	04-OCT-1999;	99US-0157117.					
PR	05-OCT-1999;	99US-0157753.					
PR	06-OCT-1999;	99US-0157865.					
PR	07-OCT-1999;	99US-0158029.					
PR	08-OCT-1999;	99US-0158232.					
PR	12-OCT-1999;	99US-0158369.					
PR	13-OCT-1999;	99US-0159293.					
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PR	14-OCT-1999;	99US-0159329.					
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PR	14-OCT-1999;	99US-0159637.					
PR	14-OCT-1999;	99US-0159638.					
PR	18-OCT-1999;	99US-0159584.					
PR	21-OCT-1999;	99US-0160741.					
PR	21-OCT-1999;	99US-0160767.					
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PR	21-OCT-1999;	99US-0160814.					
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PR	22-OCT-1999;	99US-0160980.					
PR	22-OCT-1999;	99US-0160981.					
PR	22-OCT-1999;	99US-0160989.					
PR	25-OCT-1999;	99US-0161404.					

Oy	1162	CTGTAATTCAGTAAAGCTACCTTCCCTGG--AAATTAACATTAGCCTCTTAAGT	1218
Db	1349	AGGAATATGCAAAATCCGAATCCCTGGTTTAGTGCACCGTCAAAAGTCAAGCTTTTAGAG	1408
Oy	1219	TGGTGTGGAAGCAAGCTTATATGTTATTAACAACGTGTGTAGTATGATATTCCTTTCT	1278
Db	1409	CAGTTTACCGAAGCGGGTTTGTGGTTTAGCACATGTGATTCATCTTATCCGTTT	1468
Oy	1279	TGAAGCGATCTTAGCTTTATGGAGCAGCTTCCTCGACCTTAAAGGTTATTTC	1338
Db	1469	TCAACACGCTGTAGAGATTTTAGGTGCGTTAGGGTTTGGCTTTGACGGTTTACCTTC	1528
Oy	1339	CTGTGAGATGCACTTGGCAAAACCAAGATTAAAGATCTGTGATAGTATTCGC	1398
Db	1529	CGGTGAGATGTATTTAAGACAGAGAGGTTGAGAGATGAGATGAATGGGTTTGTTC	1588
Oy	1399	TGAATACATGTGCATATTTGTTGTTATGCTTCGCTCTTATAGTCAGCCGGAATTCATGG	1458
Db	1589	TGCAAGATGTTGAGCTGTGGTTGTTTATATCATCGTTGGTCCGGAGTTGGCTCATGCG	1648
Oy	1459	CAGGACTTATTAATGATGTCAAAACCTACAGCCCTTCCGACATA	1503
Db	1649	CCGAGATTAATGCTAGACCTTAAAGGTTTACAGCCGCTTACAGACTTA	1693

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PR	27-JUL-1999;	99US-0145918.
PR	27-JUL-1999;	99US-0145919.
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PR	03-AUG-1999;	99US-0147039.
PR	04-AUG-1999;	99US-0147204.
PR	04-AUG-1999;	99US-0147302.
PR	05-AUG-1999;	99US-0147192.
PR	05-AUG-1999;	99US-0147260.
PR	06-AUG-1999;	99US-0147303.
PR	06-AUG-1999;	99US-0147416.
PR	09-AUG-1999;	99US-0147493.
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PR	18-AUG-1999;	99US-0149426.
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PR	23-AUG-1999;	99US-0149902.
PR	23-AUG-1999;	99US-0149930.
PR	25-AUG-1999;	99US-0150566.
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PR	27-AUG-1999;	99US-0151065.
PR	27-AUG-1999;	99US-0151066.
PR	27-AUG-1999;	99US-0151080.
PR	30-AUG-1999;	99US-0151303.
PR	31-AUG-1999;	99US-0151438.
PR	01-SEP-1999;	99US-0151930.
PR	07-SEP-1999;	99US-0152363.
PR	10-SEP-1999;	99US-0153070.
PR	13-SEP-1999;	99US-0153758.
PR	15-SEP-1999;	99US-0154018.
PR	16-SEP-1999;	99US-0154039.
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PR	28-SEP-1999;	99US-0156458.
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PR	04-OCT-1999;	99US-0157117.
PR	05-OCT-1999;	99US-0157753.
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PR	26-OCT-1999;	99US-0161361.
PR	28-OCT-1999;	99US-0161920.
PR	28-OCT-1999;	99US-0161992.
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Query Match 30.1%; Score 507.2; DB 21; Length 1794;		
Best Local Similarity 61.2%; Pred. No. 9.3e-143;		
Matches 837; Conservative 0; Mismatches 528; Indels 3; Gaps 1;		
Qy	133	CAAGAAGCTCGATGAGATGCTCGAGAGAGCGTACGGGACGTGCGCTTACGGCCAGTG 192
Db	195	CCAAGTACTTTGGACGACGCGGAAAAACAAAGAACTTTTGGACGCGGAGTG 254
Qy	193	CGCATATTATCACGGCGGTGATAGCTCCGGAGTGTGTCTTTAGCATGGGCTATAGCTC 252
Db	255	CACACATATATACGGCAGTGTAGGTTCCGGAGTTTTGTCACTAGCGTGGCTACGGCGC 314
Qy	253	AGCTTGGTTGGATCCGACGGACATCGATCTTACTCATTTTCTCGTTCACTACTTCA 312
Db	315	AGCTAGGTTGGCTCGCGGACGGTGGTGATGTTGCTTCTCTCTGCTGCTCACTATTCA 374
Qy	313	CCTCCACCATGCTTGCCGATTTGCTTACCGTGC CGGATCCCGTCA CGGAAAA CGGAAT 372
Db	375	CTTCTTCTCTTCTTGCTTGTACCGCTCCGCGACCTATCTCCGGCAAGGAAC 434
Qy	373	ACACTTACATGGACGTTGTTGATCTTACCTCGGTGAGTGGTGGTGGTGGTGGTGGAG 432
Db	435	ACACTTATATGGATGCTGTCGATCAAAATCTCGGTGGCGTGAAGTGAACGCTATGGGA 494
Qy	433	TGGCACAAATATGGAAATCTGATTGGGGTCACTGTTGGTTACACCATCACTGCTTCTATTA 492
Db	495	TTGTTCAAGTATCTTAATATCTTTGGTGTGCTATTGGCTACACAATTTGCTTCGGCTATAA 554
Qy	493	GTTTGGTAGGGTAGGGAATCGAACTGCTTCCAGGATAAGGCACACTCGCGATTTGA 552
Db	555	GCATGATGGCAATAAAGAGATCAAACTGTTTCCACAGAGTGGAGGAAAGATCCATGTC 614
Qy	553	CTATATCGAATTATCCGTATATGGCGGTTTTTGGTATCATTTCAAGTTATTCTTAGGCAGA 612
Db	615	ACATGAACAGTAATCCTTACATGATAGCTTTTGGATTAGTCCAGATTTCTATTCTCTCAGA 674
Qy	613	TCCCAAAATTCACAAGCTCTTTTCTTCCATTATGGCGGCGAGTCATGCTCTTTACTTT 672
Db	675	TTCCAGATTTTGATCAACTTTTGGTGGCTCTCAATCTCGCGCGGTTATGCTCTTCACTT 734
Qy	673	ATGCAACTATTGGAATTCGGTCTAGCCATCGCAACCGCTCGAGGTGGGAAAGTGGTGAAGA 732
Db	735	ATTCTCAGCGGCTCGCCCTCGGCATAGCCCAAGTTGCTGTTAATGGGAAGTGAAG 794
Qy	733	CGAGTATGAGGGCACAGCGGTTGGAGTAGATGTAAACCGAGCTCAAAAGATATGGAGAT 792
Db	795	GAAGTCTCACTGGGATTAGCATAGGACGCA---GTAACAGAGACACAGAAGATATGGAGGA 851
Qy	793	CGTTTCAAGCGGTTGGGACATAGCGGTTTCGCTATGCTTATGCCCACCGTTTCTCATCGAGA 852
Db	852	CTTTTCAAGCTCTTGAGACATGCTTTTGTCTTACTCTTACTTCACTTATCTCATCGAGA 911
Qy	853	TTGAGGTACTAGATCTAGCCGAGCTGAGAACAAAGCCAGTCAAAAGAGCGAGTCTTG 912
Db	912	TTGAGGACAGTGAAGTCAACCATCAGAAAGAGAGACGATGAAGAAGGCAACTTG 971
Qy	913	TGGAGGTATCAACCACTCTTTTCTATACATCTTTATGTTGATGTCATCGGCTATGCTGCAT 972
Db	972	TGAGCGTCAAGTGAACGACTATGTTCTATATGTTGTGTTGATGATGAGGATATGAGCCT 1031
Qy	973	TTGGAACAATGCCCTCGAGATTTCTTCAGAGATTTGGGTTTTTCGAGCCCTTTTGGC 1032
Db	1032	TTGGAGACTTGTCTCCCGAAATCTCTTAAACCGGTTTCGGGTTTTTATATATCTTATTTGGC 1091



QY 1033 TCATTGACCTTGGAAAAGCTTGATCGCTGCACCTTATGGTGCCTATCAGGTTGCG 1092  
DB 1092 TTCTTGACATTGCGAAAGCAGCCATTTGATTCACCTTATGGTGCATACCAAGTCTATT 1151  
QY 1093 GCGACCGCATATTCGACTTTGGTGAAGAAAAATGCAGAAACTATCCAGACAACAGT 1152  
DB 1152 GCCAACCTCTGTTGGCTTTCATGAGAGACAGCTTCGATTCGATTCCTCATATGAGT 1211  
QY 1153 TCATCAGCTTCGATATTCAGTAAAGCTTCCTTGGGAAATTCACATTCGCCCT 1212  
DB 1212 TCATTCGAAAAAGATATACAAATTCGATTCCTGTTTCAAGCCTCTCCGCTTGAATGCT 1271  
QY 1213 TCAGATTGGTGTGAGAGACAGCTTATGTGGTTAATACCATCTTGTAGCTATGATTC 1272  
DB 1272 TCAGTTGATATGAGAGACAGTGTGTGTGATCATACGACAGTATCTCAATGCTTCTTC 1331  
QY 1273 CTTTCTTCAACCGCATCTTGTAGTCTTATCGGAGCAGCTTCCTTGGGCTTTAAGGTTT 1332  
DB 1332 CGTTTTCACGACGTTGTGGGTCTGCTGGGGCACTAGGGTTTGGCCATTGAAGGTTCT 1391  
QY 1333 ATTTCCCTGTGAGATGCACATTCACAAACCAAGATTAAAGTACTCTGCTAGATGA 1392  
DB 1392 ATTTCCAGTGCAGAAATGTACATCGCCAGAGAGATACCTAGATGAGACACAGATGG 1451  
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RESULT 5  
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ID AAC36303 standard; DNA; 1759 BP.

AC AAC36303;  
AC 17-OCT-2000 (first entry)  
XX DE Arabidopsis thaliana DNA fragment SEQ ID NO: 13296.  
XX  
XX Hybridisation assay; genetic mapping; gene expression control;  
KM protein identification; signal transduction pathway;  
KM metabolic pathway; promoter; termination sequence; ss.  
XX  
OS Arabidopsis thaliana.  
XX  
XX EPI033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-0301439.  
XX  
XX 25-FEB-1999; 99US-0121025.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
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PR 29-MAR-1999; 99US-0126785.  
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PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
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PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145088.

PR	22-JUL-1999;	99US-0145085.	PR	21-OCT-1999;	99US-0160768.	
PR	22-JUL-1999;	99US-0145087.	PR	21-OCT-1999;	99US-0160770.	
PR	22-JUL-1999;	99US-0145089.	PR	21-OCT-1999;	99US-0160814.	
PR	22-JUL-1999;	99US-0145132.	PR	21-OCT-1999;	99US-0160815.	
PR	23-JUL-1999;	99US-0145145.	PR	22-OCT-1999;	99US-0160980.	
PR	23-JUL-1999;	99US-0145218.	PR	22-OCT-1999;	99US-0160981.	
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PR	26-JUL-1999;	99US-0145276.	PR	25-OCT-1999;	99US-0161404.	
PR	27-JUL-1999;	99US-0145913.	PR	25-OCT-1999;	99US-0161405.	
PR	27-JUL-1999;	99US-0145918.	PR	25-OCT-1999;	99US-0161406.	
PR	27-JUL-1999;	99US-0145919.	PR	26-OCT-1999;	99US-0161359.	
PR	28-JUL-1999;	99US-0145951.	PR	26-OCT-1999;	99US-0161360.	
PR	02-AUG-1999;	99US-0146388.	PR	28-OCT-1999;	99US-0161361.	
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PR	03-AUG-1999;	99US-0147038.	PR	28-OCT-1999;	99US-0161992.	
PR	04-AUG-1999;	99US-0147204.	PR	28-OCT-1999;	99US-0161993.	
PR	05-AUG-1999;	99US-0147302.	PR	29-OCT-1999;	99US-0162142.	
PR	05-AUG-1999;	99US-0147192.	Query Match 29.8%; Score 501.6; DB 2i; Length 1759;			
PR	06-AUG-1999;	99US-0147260.	Best Local Similarity 61.1%; Pred. No. 4.6e-141;			
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PR	09-AUG-1999;	99US-0147493.	DB	220	AAATGCTTCGATGATGCGCCCTCAAAGAATCGGACTGTTGGACCGCAGCGT 279	
PR	10-AUG-1999;	99US-0147935.	QY	195	CATATATACGGCGGTGATAGGCTCCGGAGTGTGCTTTTAGCATGGGCTATAGCTCAG 254	
PR	11-AUG-1999;	99US-0148319.	DB	280	CATATAATAACTCGCGTTATCGGATCCGGCGTTTTGTCAATGGCGGTGGCGGATTGCACAG 339	
PR	12-AUG-1999;	99US-0148341.	QY	255	CTTGTTGGATCGAGGACATCGATCTTACTCATTTTCTGTTTCATTACTTACTTTCACC 314	
PR	13-AUG-1999;	99US-0148565.	DB	340	CTCGATGGATCGCTGGCCCTGCTGTGATGCTATTGTTCTCTCTTGTTACTCTTTACTCC 399	
PR	13-AUG-1999;	99US-0148684.	QY	315	TCCACCATGCTTCCGATCTTACCGTGGCGGATCCGTCACCGGAAACCGAATATAC 374	
PR	16-AUG-1999;	99US-0149368.	DB	400	TCCACACTTTTAGCGACTGCTACAGAAACCGCGCATCGAGTCTGCGAAGAGAAAATAC 459	
PR	17-AUG-1999;	99US-0149175.	QY	375	ACTTACATGGACGTTGTTCCGATCTTACCTCGTGGTAGGAAAGTCAGAGTCTCTGGAGTG 434	
PR	18-AUG-1999;	99US-0149426.	DB	460	ACTTACATGGATCGCTGGCCCTTCGATCAATTTCTCGTGGGTTCAAGTTTCTGGGGTTG 519	
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PR	20-AUG-1999;	99US-0149723.	DB	520	ATTCAATACTTGAATCTCTTTGTTATCGCAATTTGGATACAGATAGCAGCTTCCCATPAGC 579	
PR	20-AUG-1999;	99US-0151303.	QY	495	TTGTTAGCGGTAGGGAAATCGAACTGCTTCCACGATAAAGGCGACACTCGGGATTTCTACT 554	
PR	31-AUG-1999;	99US-0151438.	DB	580	ATGATGGGATCAAGAGATCCAACTGCTTCCACAAGAGTGGAGGAAAGACCCCATGTCA 639	
PR	01-SEP-1999;	99US-0151930.	QY	555	ATATCGAATATCCGTATATGGCGGTTTTTGGTATCATTTCAAGTTATTCTTAGCCAGATC 614	
PR	07-SEP-1999;	99US-0152363.	DB	640	ATGTCCAGTAATCTTTACATGATGCTATTTGGTGTGCGAGAGATCTTGGTCTCTCAGGTT 699	
PR	10-SEP-1999;	99US-0153070.	QY	615	CCAAATTTCCACAAGCTCTCTTTTCTTTCCATTTATGSCCGCAGTCATGTCCTTTTACTTAT 674	
PR	13-SEP-1999;	99US-0153758.	DB	700	CCTGATTTTCGATCAGATTTGGTGGATCTCCCATTTGTCAGCTGTTATGTCCTTTCACTTAC 759	
PR	15-SEP-1999;	99US-0154018.	QY	675	GCAACTATTGGAAATCGGTCTAGCCATCCGACCGTCCGAGGTGGGAAAGTGGGTAGACG 734	
PR	16-SEP-1999;	99US-0154039.	DB	760	TCTGCCATTGGTCTAGCTCTTTGGAATCGTTCAAGTTTGACGGAATGAGGTTTTTCAANGGA 819	
PR	20-SEP-1999;	99US-0154779.	QY	735	AGTATGACGGGCACACGGGTTGGAGTAGATGTAAACCCAGCTCAAAGATATGAGATCG 794	
PR	22-SEP-1999;	99US-0155139.	DB	820	AGTCTCACTGGAATAAGCATCGGAACA---GTGACTCAAACACAGAAGATATGAGAACCC 876	
PR	23-SEP-1999;	99US-0155486.	QY	795	TTTTCAAGCGGTTGGGACATAGCGTTCCGCTTATGCTTATGCCAGGTTCTCATTCGAGATT 854	
PR	24-SEP-1999;	99US-0155659.	DB	877	TTCCAGCACTTGGAGACATTCGCTTTGCGTACTCATCTACTCTGTTGCTCTATTCGAGATT 936	
PR	28-SEP-1999;	99US-0156458.	QY	855	CAGATACACTAAGATCTTAGCCAGCTGAGAACAAAGCCATGAAAGAGCAAGTCTTTGTG 914	
PR	29-SEP-1999;	99US-0156596.	DB	937	CAGGATCTGTAAGATCCCCACCGCGGGAATCGAAACGATGAGAAAGCAACAAAATC 996	
PR	04-OCT-1999;	99US-0157117.	QY			
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Oy	915	GGAGTATCAACCAACCACTTTTCTACATCTTAATGAGATGATCGCTATGCTGATTT	974
Db	997	AGATTGCGGTACAAACATATTTCTACATGCTATGAGGTATGAGCGCTTTT	1056
Oy	975	GGAAACAATGCCCTGGAGATTTCTTACAGATTTGGGTTTTCAGACCTTTTGGCTC	1034
Db	1057	GGAGATGACGACACGGGAAACCTCTCCACGGGTTTGGATTCTCAACACCGTTTGGCTC	1118
Oy	1035	ATTGACTTTGGAAAGCTTGTGATGCTGTCTCACTTAATGGTGCCTATCAAGTGTTCGCG	1094
Db	1117	CTTGACATAGCTAAAGCGCGCATTTGTGTCACTGTGTGAGCTTACAAAGCTTTGTGT	1176
Oy	1095	CAGCCGATTTTCCAGTTGTTGGAGAAAATGACAGAAACTATCCAGACAAAGTTTC	1154
Db	1177	CACCCCATCTTGGCCCTTAATGAAAATCAGTGCAGAGAGATATCCAGCAATGACTTC	1236
Oy	1155	ATCATCTTGAATATTCTAGTAAAGTAC--TTTCTTGGAAAATTCAACATTAGCTTC	1211
Db	1237	CTACGACAGAGATTTGAAATCAGATCCCGGATTTAACTCTCTTAAGAAAGTAAGTT	1296
Oy	1212	TTCAAGTTGGTGGAGACAGCTTATGAGTTATTAACACTGTTGTAAGCTATGATATTC	1271
Db	1297	TTGAGATGATTTTACAGAGAGTGGCTTGTGTGTTACAAACCACTGATATAGATGCTGATG	1356
Oy	1272	CTTTTCTCAACGCGCATCTTAAAGTCTTATGAGAGCAGCTTCTCTGAGCTTTAACGGTT	1331
Db	1357	CCGTTTTTTAAAGAGCGGTGGGATCTTAAAGGGCGTTAGGGTTTGTGCTTGAAGGTT	1411
Oy	1332	TATTTCCCTGGAGATGCACATTTGCACAAACCAAGATTAAAGAGTACTGTCTAATGG	1399
Db	1417	TATTTTCCGGTGAATATTAATTAAACAGAGAGAGTGGAGAAATGAGACGAAATGG	1476
Oy	1392	ATTGACCTGAAAAAGATGCTATGTCTTGTGCTTATGCTGCTGCTTATGAGTGCAGCGGA	1451
Db	1477	GTGTGTTTACAGATGCTTACGTGTGCTTGTGTGTATCTCGTGGTGTGCGGGGTATGGA	1533
Oy	1452	TCCATGCGACGACTTATAAGTAGTGCAAAACCTACAGCCCTTCGGACTATGATGAG	1511
Db	1537	TCATATGCGGAGATGATCTTGATCTTAAGTCTTAATAGCCATTCAGTCTAATATGTA	1596
Oy	1512	TGAGTTTG 1519	
Db	1597	TGATTATG 1604	
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AC			
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DT	17-OCT-2000 (first entry)		
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De	Arabidopsis thaliana DNA fragment SEQ ID NO: 32189.		
XX			
KM	Hybridisation assay; genetic mapping; gene expression control;		
KX	protein identification; signal transduction pathway;		
KW	metabolic pathway; promoter; termination sequence; ss.		
XX			
OS	Arabidopsis thaliana.		
XX			
PN	EP1033405-A2.		
XX			
PD	06-SEP-2000.		
XX			
PF	25-FEB-2000; 2000EP-0301439.		
XX			
PR	25-FEB-1999; 99US-0121825.		
PR	05-MAR-1999; 99US-0121180.		
PR	09-MAR-1999; 99US-0123548.		
PR	23-MAR-1999; 99US-0125788.		
PR	25-MAR-1999; 99US-0126264.		

PR	20-MAR-1999	99US-0126785
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PR	06-APR-1999	99US-0128234
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PR 20-JUL-1999; 99US-0144352.  
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PR 23-JUL-1999; 99US-0145224.  
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PR 23-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149930.  
PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 27-AUG-1999; 99US-0151065.  
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PR 27-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
PR 15-SEP-1999; 99US-0154018.  
PR 16-SEP-1999; 99US-0154039.  
PR 20-SEP-1999; 99US-0154779.  
PR 22-SEP-1999; 99US-0155139.  
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PR 24-SEP-1999; 99US-0155659.  
PR 28-SEP-1999; 99US-0156458.  
PR 29-SEP-1999; 99US-0156596.  
PR 04-OCT-1999; 99US-0157117.  
PR 05-OCT-1999; 99US-0157753.  
PR 06-OCT-1999; 99US-0157865.  
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PR 12-OCT-1999; 99US-0158369.  
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PR 28-OCT-1999; 99US-0161920.  
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PR 29-OCT-1999; 99US-0162142.  
  
Query Match 26.4%; Score 445.4; DB 21; Length 1375;  
Best Local Similarity 61.8%; Pred. No. 4.3e-124;  
Matches 726; Conservative 0; Mismatches 446; Indels 3; Gaps 1;  
  
Qy 133 CAAAGAACGTCGATGAAGATGGTCGAGAGAACGCTACCGGACGTGGCTTTACGGCGAGTG 192  
Db 194 CCAAGTACTTTGGACGACGCGGAAACAAAGAACTGGGAGTGTTCGACGCGAGTG 253  
Qy 193 GCGATATTATCAGCGGGGTAGAGTCCGGAGTGTCTTTAGCATGGGCTATAGCTC 252  
Db 254 CACATAATACGGCAGGTAGGTTCGGAGTGTTCGACTAGCTGGGCTACGGCGC 313  
Qy 253 AGCTTGGTGGATCGCAGGACATCGATCTTACTCATTTTCTCGTTCACTTACTTCTCA 312  
Db 314 AGCTAGTTCGGCTCGCGGACCGGTGGTGTGTTGCTCTCTCTGCGCTCACTATTTC 373  
Qy 313 CCTCCACCATGCTTCGGATTCCTACCGTGGCGCGGATCCGTCACCGGAAAGCAAT 372  
Db 374 CTTCCTCTCTTCGCTGCTTTTACCGCTCGCGGACCTATCTCCGCAAGGAACT 433  
Qy 373 ACCTTACATGGACGTTGTTTCGATCTTACCTCGGTGGTAGGAAAGTGCAGCTCTGTGG 432  
Db 434 ACCTTATATGGATGCTGTCGATCAAAATCTCGGTGGCGTGAAGGTGACCTATGTGG 493  
Qy 433 TGGCACAATATGGGAATCTGATGGGGTCACTGTTGGTTACACCATCACTGCTTCTAT 492  
Db 494 TTGTTTCAGTATCTTAATACTTTGGTGTGTTGTTGGTACACAAATGCTTCGGCTATA 553  
Qy 493 GTTTGGTAGCGGTAGGGAATCGAACTGCTTCCACGATAAAGGCACTCGCGGATTTGA 552  
Db 554 GCATGATGGCAATAAAGAGATCAAACTGTTTCCACAGAGTGGAGGAAAGATCCATGTC 613  
Qy 553 CTATATCGAATATACGATATAGCGGTTTGGTGTATCATTCAGTTATTTTAGCCAGA 612  
Db 614 ACATGAAACAGTAATCTTACATGATAGCTTTTGGATAGTCCAGATTCATATCTCTCA 673  
Qy 613 TCCCAAAATTTCCACAAGCTCTCTTTTTCATTTATGGCGGAGTCACTGCTTTTACTT 672  
Db 674 TCCAGATTTTGGATCAACTTTGGTGGCTCTCAATCCTCGCGCGTATATGCTCTTCACT 733  
Qy 673 ATGCACTATTGGAATCGGCTAGCCATCGGAAACCGTCGCGAGTGGGAAAGTGGTA 732  
Db 734 ATTCCTCAGCCGGTCTCGCCCTCGGCTAGCCAAAGTTGTCGTTAATGGGAAGGTGAAG 793





Qy	817	CGTGGCCATGCTTAAAGCAGCGTTCATGACATTCAGAGTACATGAATCTAGCGC	876
Db	728	CGTTTCAATCTCTTTTCATCATCTACTTTGAGATTCAGAGACATGAGTACACAC	787
Qy	877	CAGCTGAGAACAAAGCCATGATAAAGAGCAAGCTTTGTGGAGATTCACACACATTTT	936
Db	788	CGGACAGAGAGCAACATATATAAAGAGCTCGACGTTGTGGATTTTATCAAACTTCT	847
Qy	937	TCTACATCTTATGTGATGATCGGCTATGCTGATTCATTTGAAACATAGCCCTGAGATT	996
Db	848	TCTTCTCTGTTGTGATGATTTTGGGATAGCGGCTTTTGGAGATTCACCCGGGAAATC	907
Qy	997	TGCTCAAGATTTTGGGTTTTTGAGCCCTTTTGGCTATTTGATCTTTGCAAAAGCTTGA	1058
Db	908	TCTTGAACGGTTTGCGCTTCTATGAGCACATTCGCTGTGTGATTTGCGCAAGCTTGA	967
Qy	1057	TGCTGTCCACCTTATTTGATGATCGCTATCAGTGTGTCGCGACCGCATATTCAGTTGTG	1116
Db	968	TGTTCTTCATTTGTTGGTGGATTCAGGTATACAGTCAACAAATTTTGCGGCTGCGG	1027
Qy	1117	AGAAAAATGCAACAGAACTATTCACAGACAAAGTTGATGATCTTGGAAATTTCAGTAA	1178
Db	1028	AGAGATCGCTACCAAGAAATATCCGAAAAATAGTTTATGCGCAATCTACGGATTGA	1087
Qy	1177	ACGTACCTTTCCTTGA-----AAATTCAATTAGCCTCTTCAGATTGTGTGAGGA	1230
Db	1088	AACCTCCATTTGCTCGAGAGAGACGCTGAGATTGAACCAATAGAGATGTGTTTGAGA	1147
Qy	1231	CAGCTTATGTGGTTATTAACACTGTTTGAAGTATGATATCCCTTTTCAAGCGATAT	1290
Db	1148	CGATGTACGTGTGATACACACGGAGATGGCAGTATATTTCCCTTACTTCAATGAAGTAT	1207
Qy	1291	TAGGTCTTATGAGAGCAGCTTCCTTCGACCTTTAAACGTTTATTTCCCTGTGAGATGC	1350
Db	1208	TAGGAGTGTGTGGGGCACTTGCAATTTTGGCTCTGTGACGTATATTTTCTGTGAGATGT	1267
Qy	1351	ACATTGACAAACCAAGATTAAAGAGTACTGTGATAGATTTGGCTGAAGAACATGT	1410
Db	1268	GTATATTTGAGAGAAATCCGAAGTTGACCGCAGCATGCTCTTTAGAGTTTCA	1322
Qy	1411	GCTATGTTTCTTGTATGCTCTCGCTGTAACTGACGCCGATCATGCGACAGACTTAT	1468
Db	1328	GCTTGTGTGCTGTGCTGTGCTCTGTGCTCTTGTGTTGATCTAATTATGAGACTTGT	1385
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ABQ65898			
ID	ABQ65898	strand; DNA, 660 BP.	
AC	ABQ65898;		
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XX	21-AUG-2002 (first entry)		
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XX	Arabidopsis thaliana polynucleotide SEQ ID NO 475.		
XX			
XX	Arabidopsis thaliana; thale cress; plant; transgenic; GMO; disease;		
XX	stress; metabolic pathway; biosynthetic pathway; nutrition; fungicide;		
XX	insecticide; antibiotic; ds.		
XX			
OS	Arabidopsis thaliana.		
XX			
XX	US2002059663-A1.		
XX			
XX	16-MAY-2002.		
XX			
XX	26-JUN-2001; 2001US-0770149.		
XX			
XX	27-JUN-2000; 2000US-178506P.		
XX			
XX	(GORL/) GORLACH J.		
XX	(ANY/) AN Y.		
XX	(HAMI/) HAMILTON C M.		

XX	(PRIC/) PRICE J L.
PA	(RAIN/) RAINES T M.
PA	(YUYU/) YU Y.
PA	(RAME/) RAMEKA J G.
PA	(PAGE/) PAGE A.
PA	(MATH) MATHEW A V.
PA	(LEDF) LEDFORD B L.
PA	(WOES) WOESSNER J P.
PA	(HAAS/) HAAS W D.
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PA	(KRICK) KRICKER M.
PA	(SLAT/) SLATER T.
PA	(DAVI/) DAVIS K R.
PA	(ALLE/) ALLEN K.
PA	(HOFF) HOFFMAN N.
PA	(HURB) HURBAN P.
XX	Goriach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y;
P1	Rameka JC, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;
P1	Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N;
P1	Hurban P;
XX	
DR	WP1; 2002-479224/51.
XX	
PT	New nucleic acid that hybridizes to Arabidopsis thaliana sequences,
PT	useful e.g. for preparing transgenic plants with increased resistance
PT	or altered metabolism -
PS	
PS	Claim 1; SEQ ID NO 475; 40bp + Sequence listing; English.
CC	
CC	The invention relates to nucleic acids (I) that hybridise under stringent
CC	conditions to any of 999 sequences (AB065424-AB066422) or their
CC	fragments. (II) are used to express the corresponding polypeptides (II) or
CC	to produce genetically modified plant cells or transgenic plants, which
CC	may have improved resistance to disease or stress, or altered
CC	metabolic/biosynthetic pathways (for production of commercial,
CC	nutritional or medicinal products), or generally any trait of interest,
CC	or can be used to screen for biologically active agents (e.g. fungicides,
CC	insecticides and antibiotics).
CC	Note: The sequence data for this patent did not form part of the printed
CC	specification, but was obtained in electronic format directly from the
CC	USPTO at seqdata.uspto.gov/sequence.html?docID=99909770149.
SQ	Sequence 660 BP; 179 A; 118 C; 165 G; 198 T; 0 other;
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DB	61 ATTCTGCGCTTAATTTAGAACACAGCTGCGCTTAGTTTCCGACAGTGACTTGGTACC 180
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DB	181 AAGGAATACGAATATCGAATCCCTGTTTTAGGTACACCGGTACAAAGTATTCAGA 240
OY	1218 TTGGTGGGAGGACAGCTAATGTGTTATACACTGTGTACTATGATATTCCTCTTC 1277
DB	241 GCAGTTTACCGAAGCGGTTGTGTTTATGACACTGTATATCACTGCTTATGCCGTTT 300
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KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
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KW	Hybridisation assay; genetic mapping; gene expression control;		
KW	protein identification; signal transduction pathway;		
KW	metabolic pathway; promoter; termination sequence; ss.		
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PR 29-OCT-1999; 99US-0162142.
Query Match 4.5%; Score 76; DB 21; Length 485;
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Matches 121; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

OY 166 GTACCGGAGCGTGGCTTACGCGAGTGGCGATATATATCAACGCGGTGATAGCTCCGAG 225
DB 120 GACAGGAGCGTATGAGACGGGTGGACATATATATACAGAGTGAATAGAGCTGAG 179
OY 226 TGTGTCTTATGATAGGCTATAGCTTACAGTGTGGATGGCAGGAGCATGATCTTAC 285
DB 180 TGTGTGTGTGGCTGGCCACGCGAGCTGGGTGATGCTGTCCGCGCCCTTA 239
OY 286 TCATTTCTGCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 345
DB 240 TAGCTTGGCGGGGTGACACTCTCTGCTTTCTTCTTCCGATTGCTACGCTTCC 299
OY 346 CGGATCCCGTCACCGG 361
DB 300 CTGATCCTTAACACGG 315

RESULT 11
AAD02471
ID AAD02471 standard; cDNA; 1882 BP.
AC AAD02471;
XX
XX 24-APR-2001 (first entry)
DE cDNA clone bsh1.pk0013.h9, encoding barley LHT1.
XX
XX Barley; lysine- and histidine-specific transporter; LHT1;
KW proline transporter; transgenic plant; immunological screening; ss.
XX
XX Hordeum vulgare.
OS
XX
XX Key Location/Qualifiers
XX CDS 70..1413
XX FT /*tag= a
XX FT /product= "barley LHT1 protein"
XX
XX US6165792-A.
XX
XX 26-DEC-2000.
XX
XX 09-AUG-1999; 99US-0370253.
XX
XX 20-AUG-1998; 98US-0097222.
XX
XX (DUBO ) DU PONT DE NEMOURS & CO E I.
XX
XX Thopre CJ, Allen SM;
XX
XX WPI; 2001-090485/10.
XX P-PSDB; AAY72391.
XX
XX Nucleic acids encoding amino acid transporters, e.g. lysine- and
XX histidine-specific transporter and proline transporter, useful for
XX transgenic plant production with altered expression level of the amino
XX acid transporters -
XX
XX Claim 3; Column 19-22; 24pp; English.
XX
XX The present cDNA sequence encodes barley lysine- and histidine-specific
XX transporter (LHT1) from clone bsh1.pk0013.h9, isolated from a barley
XX sheath or developing seedling tissue of bsh1 cDNA library.
XX
XX The invention relates to lysine- and histidine-specific transporter
XX (LHT1), proline transporter and their corresponding cDNA clones. It is
XX useful for producing transgenic plants with altered expression level of
XX amino acid transporters, in cell types or developmental stages in which
XX they are not normally found, such that the obtained transgenic plants

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CC show increased tolerance to salt and water stress. The level of lysine,
CC histidine and proline in cells of the transgenic plant, is also altered.
CC The invention is also used for constructing a chimeric gene encoding all
CC or a portion of the amino acid transporter, where in the expression of
CC chimeric gene results in the production of altered levels of amino acid
CC transporter in a transformed host cell. Synthetic peptides obtained from
CC LHT1 and proline transporter are used for immunising animals to produce
CC polyclonal or monoclonal antibodies, which facilitates the immunological
CC screening of cDNA expression libraries.
XX
XX Sequence 1882 BP; 475 A; 488 C; 466 G; 453 T; 0 other;
SQ
Query Match 3.2%; Score 53.2; DB 22; Length 1882;
Best Local Similarity 51.1%; Pred. No. 3.7e-05;
Matches 183; Conservative 0; Mismatches 163; Indels 12; Gaps 2;

OY 768 ACCGAGCTCAAAAGATATGAGATGCTTCAAGCGGTGGGAGCATGCGCTTAT 827
DB 730 ACGACGACGAGGCGAGCTTTGCTTTCTTGGGGGCGCTCGGAGATGTGCAATTCCTAC 789
OY 828 GCTTATGCGACGTTCTCATGAGATTCAAGATACATTAAGATTAGCTCAG-----CT 881
DB 790 TCCGCGCACATGTGTGTCTAGAAATTCAGGCTACCATCCATCGACCGCGCAACCG 849
OY 882 GAGAAACAAAGCCATGAAAGAGCAAGTCTTGGAGATATCAACACCATTTTCTTAC 941
DB 850 TCCAAAGAGCCAAATGTGAAAGGCGGTGTGCTTACATCATATGCGCGCTGCTAC 909
OY 942 ATCTTATGTGATGATGATGCTATGCTGATTTGAAACAAATGCCCTTGAGATTCTCTC 1001
DB 910 TTCCCGGTGGCATTTATCGGCTACTGGGCAATTTGGCAACAGCGTGACAGCAACATCTCTC 969
OY 1002 ACAGATTTGGGGTTTGGAGCCCTTTGGCTTATGATGATTTGCAAAAGCTTGTGCT 1061
DB 970 A-----TCACCTTCAACAAAGCCCAAGTGGCTTATGCTATGCCCAACATGATGTCTC 1023
OY 1062 GTCCACCTTATGTGGCTTATCAAGTGTGTGGCGACCGCATATTCAGTGTGTTGAGA 1119
DB 1024 GTTCACCTCATCGGTAGCTACCAAGATTATGCGATGCCGTGTGTGACATGTGAGA 1081

RESULT 12
AAD02472
ID AAD02472 standard; cDNA; 1016 BP.
AC AAD02472;
XX
XX 24-APR-2001 (first entry)
DE cDNA clone ctain.pk0048.h2, encoding corn LHT1.
XX
XX Corn; lysine- and histidine-specific transporter; LHT1;
KW proline transporter; transgenic plant; immunological screening; ss.
XX
XX Zea mays.
XX
XX Key Location/Qualifiers
XX CDS 2..781
XX FT /*tag= a
XX FT /product= "Corn LHT1 protein"
XX FT /note= "Does not include start codon"
XX FT /partial]
XX
XX US6165792-A.
XX
XX 26-DEC-2000.
XX
XX 09-AUG-1999; 99US-0370253.
XX
XX 20-AUG-1998; 98US-0097222.
XX
XX (DUBO ) DU PONT DE NEMOURS & CO E I.
XX

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PI Thopre CU, Allen SM;  
XX WPI: 2001-090485/10.  
XX P-PSDB; AAY72392.  
XX Nucleic acids encoding amino acid transporters, e.g. lysine- and  
PT histidine-specific transporter and proline transporter, useful for  
PT transgenic plant production with altered expression level of the amino  
PT acid transporters -  
XX  
XX  
XX Claim 3; Column 23-26; 24pp; English.  
XX  
XX The present cDNA sequence encodes corn lysine- and histidine-specific  
CC transporter (LHT1) from clone ctan.pk0048.h2, isolated from a corn  
CC tissue ctan cDNA library.  
XX The invention relates to lysine- and histidine-specific transporter  
CC (LHT1), proline transporter and their corresponding cDNA clones. It is  
CC useful for producing transgenic plants with altered expression level of  
CC amino acid transporters, in cell types or developmental stages in which  
CC they are not normally found, such that the obtained transgenic plants  
CC show increased tolerance to salt and water stress. The level of lysine,  
CC histidine and proline in cells of the transgenic plant, is also altered.  
CC The invention is also used for constructing a chimeric gene encoding all  
CC or a portion of the amino acid transporter, where in the expression of  
CC chimeric gene results in the production of altered levels of amino acid  
CC transporter in a transformed host cell. Synthetic peptides obtained from  
CC LHT1 and proline transporter are used for immunising animals to produce  
CC polyclonal or monoclonal antibodies, which facilitates the immunological  
CC screening of cDNA expression libraries.  
XX  
XX Sequence 1016 BP; 203 A; 294 C; 269 G; 250 T; 0 other;  
XX  
XX Query Match 3.1%; Score 51.6; DB 22; Length 1016;  
XX Best Local Similarity 50.8%; Pred. No. 8.2e-05;  
XX Matches 182; Conservative 0; Mismatches 164; Indels 12; Gaps 2;  
XX  
Qy 768 ACCGACGTCAAAGATATGAGATCGTTTCAAGCGGTTGGGACATAGCGTTCCGCTAT 827  
Db 98 ACCAGCGGGGAGGTGTCGGCTTCTTCGGCGGCTGGGGAGCTGGCGTTTCGCTAC 157  
Qy 828 GCTTATGCCAGGTTCTCATCGAGATTCAGGATACACTAAGATCTPAGCCAGCTGAG--- 884  
Db 158 GCCGGCCACAACTGGTGTCTGGAGATCCAGGCCACCATCCGTCACCCCGACAAAGCCG 217  
Qy 885 ---AACAAAGCCATGAAGACGACGACTTGTGGAGTATCAACACCACTTTTCTTAC 941  
Db 218 TCCAGAGGCCATGGAAGGCGGTGTGTGCGCTACGTCGTGGCGCTCTGTAC 277  
Qy 942 ATCTTATGTGATGATCGGCTATGCTGATTTGGAACAATGCCCCCTGGAGATTTCCCTC 1001  
Db 278 TTCCCCGTCGCGCTCATCGGCTACTCGGGGTTTCGGAACACAGTCGAGGACAACTCTC 337  
Qy 1002 ACAGATTTCCGTTTTCGAGCCCTTTTCGCTCATTTGCTTTCGAAAGCGTTGCATCGCT 1061  
Db 338 A-----TCAGGCTCAGCAAGCCCAAGTGGCTCATCGGCTCGCAACATGCTGCTC 391  
Qy 1062 GTCACCTTATGTGCTATACAGTGTTCGCGACGCGGATATCCAGTTTGTGAGA 1119  
Db 392 GTCCATGTCATCGGACGCTACCAAGACTATGCGATGCGCGTGTGATGATGATAGAGA 449  
XX  
XX RESULT 13  
XX AAD02473  
XX ID AAD02473 standard; cDNA; 1865 BP.  
XX  
XX AAD02473;  
XX  
XX 24-APR-2001 (first entry)  
XX  
XX cDNA clone rls48.pk0011.g8, encoding rice LHT1.  
XX  
XX Rice; lysine- and histidine-specific transporter; LHT1;  
XX proline transporter; transgenic plant; immunological screening; ss.  
KW

XX Oryza sativa.  
XX  
XX Key Location/Qualifiers  
XX CDS 112..1455  
XX /\*tag= a  
XX /product= "Rice LHT1 protein"  
XX  
XX US6165792-A.  
XX  
XX 26-DEC-2000.  
XX  
XX 09-AUG-1999; 99US-0370253.  
XX  
XX 20-AUG-1998; 98US-0097222.  
XX  
XX (DUPO ) DU PONT DE NEMOURS & CO E I.  
XX Thopre CU, Allen SM;  
XX WPI: 2001-090485/10.  
XX P-PSDB; AAY72393.  
XX Nucleic acids encoding amino acid transporters, e.g. lysine- and  
PT histidine-specific transporter and proline transporter, useful for  
PT transgenic plant production with altered expression level of the amino  
PT acid transporters -  
XX  
XX Claim 3; Column 25-28; 24pp; English.  
XX  
XX The present cDNA sequence encodes rice lysine- and histidine-specific  
CC transporter (LHT1) from clone rls48.pk0011.g8, isolated from a rice  
CC leaf tissue rls48 cDNA library.  
XX The invention relates to lysine- and histidine-specific transporter  
CC (LHT1), proline transporter and their corresponding cDNA clones. It is  
CC useful for producing transgenic plants with altered expression level of  
CC amino acid transporters, in cell types or developmental stages in which  
CC they are not normally found, such that the obtained transgenic plants  
CC show increased tolerance to salt and water stress. The level of lysine,  
CC histidine and proline in cells of the transgenic plant, is also altered.  
CC The invention is also used for constructing a chimeric gene encoding all  
CC or a portion of the amino acid transporter, where in the expression of  
CC chimeric gene results in the production of altered levels of amino acid  
CC transporter in a transformed host cell. Synthetic peptides obtained from  
CC LHT1 and proline transporter are used for immunising animals to produce  
CC polyclonal or monoclonal antibodies, which facilitates the immunological  
CC screening of cDNA expression libraries.  
XX  
XX Sequence 1865 BP; 439 A; 517 C; 472 G; 437 T; 0 other;  
XX  
XX Query Match 2.8%; Score 47.6; DB 22; Length 1865;  
XX Best Local Similarity 50.6%; Pred. No. 0.0019;  
XX Matches 175; Conservative 0; Mismatches 159; Indels 12; Gaps 2;  
XX  
Qy 780 AAGATATGGAGATCGTTTCAAGCGGTTGGGACATAGCGTTTCGCTATGCTATGCCAGC 839  
Db 784 AAGGTGTTCGGCTTCTTCAGCGCGCTGGGCGACGTCGCGTTTCGCTACGGGGGCAAC 843  
Qy 840 GTTCTCATCCGATTCAGGATACACTAAGATCTAGCCAGCTGAG-----AACAAAGCC 893  
Db 844 GTGCTGTGGAGATCAGCGGACCATCCGTCGACGCCGAGAGCGGTCACAAAGACCG 903  
Qy 894 ATGAAAGACCAAGCTTTCGGAGATATCAACACCACCTTTTCTCATCTTATGTGA 953  
Db 904 ATGGAAGGGGCGTCTGCTCGCTACATCATCTGCGGCTCTGCTACTTCCCGTGGCG 963  
Qy 954 TGCATCGGCTATGCTGCATTTGGAAACAATGCCCTTGAGATTTTCCTCACAGATTTCCGG 1013  
Db 964 CTGTCGGATACCTGGGCGTTTCGGCAACCACTGCGACGACAAACATCTCTCA-----TCACG 1017  
Qy 1014 TTTTTCGAGCCCTTTTGGCTCATTTGACTTTTGGAAACGCTTGCATCGCTGTCCACCTATT 1073  
Db 1018 CTCTCCAGGCCCAATGGCTCATCGGCTCGCAACATGATGTCGTCATCCATGTCATC 1077

OY 1074 GGTGCTATCATGGTGTTCGGCAGCGATATTCAGTTGTGAGA 1119  
DB 1078 GGGAGCTACCATCTACCGCAGCGGTGTTCAGATGATGAGA 1123

RESULT 14  
AAC52941  
ID AAC52941 standard; DNA; 61 BP.  
XX AAC52941;  
AC AAC52941;  
XX 18-OCT-2000 (first entry)  
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 72900.  
XX  
XX Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway;  
KW metabolic pathway; promoter; termination sequence; ss.  
XX Arabidopsis thaliana.  
OS  
XX EPI033405-A2.  
PN  
XX  
XX 06-SEP-2000.  
PD  
XX  
XX 25-FEB-2000; 2000EP-010139.  
PE  
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XX 25-FEB-1999; 99US-0121825.  
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PR 22-OCT-1999; 99US-0160981.  
PR 22-OCT-1999; 99US-0160989.  
PR 25-OCT-1999; 99US-0161404.  
PR 25-OCT-1999; 99US-0161405.  
PR 25-OCT-1999; 99US-0161406.  
PR 26-OCT-1999; 99US-0161359.  
PR 26-OCT-1999; 99US-0161360.  
PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161992.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.

Query Match 2.74; Score 46.2; DB 21; Length 1297;  
Best Local Similarity 62.6%; Pred. No. 0.004;  
Matches 72; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 1389 TCGATTGGCGTGAAGACGATGCTATGTTGCTGATGCTGCTCGCTTACCTGCAGACC 1448  
DB 981 TGGGTTGTCTGCAAGATGTGAGCTGTGTTGATATCACTGTTGCTCCCGAGATT 1040  
QY 1449 GCATCCATCGCAGAGACTTATTAAGTAGTGCAAAACCTACAGCCCTTCGCGACTA 1503  
DB 1041 GGCTCCATCGCCGAGAGTAATCTAGACCTTAAGATTTAACAGCCGTTCAAGACTA 1095

Search completed: December 1, 2002, 09:02:54  
Job time : 287 secs



GenCore version 5.1.3  
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OW nucleic - nucleic search, using sw model

Run on: December 1, 2002, 08:57:52 ; Search time 69 Seconds

(without alignments)  
9404.631 Million cell updates/sec

Title: US-09-854-562-1

Perfect score: 1685  
1 CTTAAACATTATTATTATC.....TTCACAAAAA

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 341543 seqs, 19255720 residues

Total number of hits satisfying chosen parameters: 663086

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1451.6	86.1	1458	9	US-09-938-842A-1470
2	722.2	42.9	1446	9	US-09-938-842A-802
3	507.2	30.1	1431	9	US-09-938-842A-67
4	501.8	29.8	1482	9	US-09-938-842A-1482
5	191.6	11.4	660	10	US-09-770-149-475
6	180	10.7	406	10	US-09-878-574-3976
7	149	8.8	382	10	US-09-878-574-2601
8	135.4	8.0	387	10	US-09-878-574-3664
9	119.8	7.1	481	10	US-09-924-035A-35
10	101.4	6.0	383	10	US-09-878-574-103
11	94.4	5.6	264	10	US-09-878-574-103
12	88.2	5.2	386	10	US-09-878-574-3794
13	88	5.2	307	10	US-09-878-574-1977
14	80	4.7	238	10	US-09-923-876-317
15	56.8	3.4	382	10	US-09-878-574-3185
16	56	3.3	2000	9	US-09-938-842A-1462
17	53	3.1	360	10	US-09-878-574-1677
18	52.4	3.1	265	10	US-09-878-574-7530
19	49.4	2.9	365	10	US-09-878-574-2526

20	48.6	2.9	322	10	US-09-878-574-2868	Sequence 2868, Ap
21	48.4	2.9	280	10	US-09-923-876-6149	Sequence 6149, Ap
22	46.6	2.8	301	10	US-09-878-574-1241	Sequence 1241, Ap
23	46.6	2.8	313	10	US-09-878-574-5166	Sequence 5166, Ap
24	44.2	2.6	376	10	US-09-878-574-4760	Sequence 4760, Ap
25	41.6	2.5	346	10	US-09-770-791-760	Sequence 760, Ap
26	41.2	2.4	159	10	US-09-878-574-9521	Sequence 9521, Ap
27	38	2.3	5005	10	US-09-764-847-1385	Sequence 1385, Ap
28	38	2.3	13831	10	US-09-764-847-1383	Sequence 1383, Ap
29	38	2.3	13832	10	US-09-764-847-1384	Sequence 1384, Ap
30	37.8	2.2	387	10	US-09-878-574-1837	Sequence 1837, Ap
31	37.6	2.2	39768	10	US-09-813-220-3	Sequence 3, Appl1
32	37.4	2.2	449	9	US-09-933-797-90	Sequence 90, Appl1
33	37.2	2.2	2833	10	US-09-925-301-204	Sequence 204, Appl
34	37	2.2	428	10	US-09-969-373-1172	Sequence 1172, Ap
35	36.8	2.2	266	10	US-09-878-574-9185	Sequence 9185, Ap
36	36.2	2.1	1272	10	US-09-765-205-9	Sequence 9, Appl1
37	36.2	2.1	1960	10	US-09-746-801A-12	Sequence 12, Appl1
38	36.2	2.1	3617	10	US-09-746-801A-14	Sequence 14, Appl1
39	35.8	2.1	310	10	US-09-923-876-3684	Sequence 3684, Ap
40	35	2.1	1813	10	US-09-732-618-9	Sequence 330, Appl1
41	35	2.1	2088	9	US-09-938-842A-330	Sequence 9, Appl1
42	35	2.1	2088	10	US-09-746-801A-4	Sequence 4, Appl1
43	35	2.1	2518	10	US-09-746-801A-1	Sequence 1, Appl1
44	35	2.1	2846	9	US-10-008-016-1	Sequence 1, Appl1
45	35	2.1	4221	10	US-09-746-801A-3	Sequence 3, Appl1

## ALIGNMENTS

RESULT 1  
US-09-938-842A-1470  
Sequence 1470, Application US/09938842A  
Patent No. US20020160378A1  
GENERAL INFORMATION:  
APPLICANT: Harper, Jeff  
APPLICANT: Kreps, Joel  
APPLICANT: Wang, Xun  
APPLICANT: Zhu, Tong  
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
TITLE OF INVENTION: SAME, AND METHODS OF USE  
FILE REFERENCE: SCRIPT300-3  
CURRENT APPLICATION NUMBER: US/09/938,842A  
PRIOR FILING DATE: 2001-08-24  
PRIOR APPLICATION NUMBER: US 60/227,866  
PRIOR FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: US 60/264,647  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/300,111  
PRIOR FILING DATE: 2001-06-22  
NUMBER OF SEQ ID NOS: 5379  
SEQ ID NO 1470  
LENGTH: 1458  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
US-09-938-842A-1470  
Query Match 86.1%; Score 1451.6; DB 9; Length 1458;  
Best Local Similarly 99.7%; Pred. No. 0;  
Matches 1454; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 57 ATGAAGATTTCACACAGACGACCAACCTCCAGCGCGAATCCGCGATCCTAC 116  
Db 1 ATGAAGATTTCACACAGACGACCAACCTCCAGCGCGAATCCGCGATCCTAC 60  
QY 117 ACCGTGTGGACCCGACAAAGACGTGAGAGTGTGAGAGAACCTTACCGGACG 176  
Db 61 ACCGTGTGGACCCGACAAAGACGTGAGAGTGTGAGAGAACCTTACCGGACG 120  
QY 177 TGGCTTACGCGAGATGCGATATTATTCACGCGCGTGTAGTCCGAGTGTCTTTA 236  
Db 121 TGGCTTACGCGAGATGCGATATTATTCACGCGCGTGTAGTCCGAGTGTCTTTA 180

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Qy 237 GCATGGGCTATAGCTCAGCTTGGTTGGATCGCAGGACATCGATCTTACTCAITTTCTCG 296
Db 181 GCATGGGCTATAGCTCAGCTTGGTTGGATCGCAGGACATCGATCTTACTCAITTTCTCG 240
Qy 297 TTGATTAATTACTTACCTCCACCATGCTTGGCGATGCTGCTACCGTGGCGGATCCCGTC 356
Db 241 TTCATTAATTACTTACCTCCACCATGCTTGGCGATGCTGCTACCGTGGCGGATCCCGTC 300
Qy 357 ACCGGAACCGAAATTACATCTTACATGAGCTTGTTCGATCTTACCTCGGTGGTAGAAA 416
Db 301 ACCGGAACCGAAATTACATCTTACATGAGCTTGTTCGATCTTACCTCGGTGGTAGAAA 360
Qy 417 GTGCAGCTCTGTGGAGTGGCAGCATATGGAATCTGATTTGGGTCACATGTTGGTTACACC 476
Db 361 GTGCAGCTCTGTGGAGTGGCAGCATATGGAATCTGATTTGGGTCACATGTTGGTTACACC 420
Qy 477 ATCACTGCTTCTATTAGTTTGGTAGCGGTAGGAAATCGAATGCTTCCACGATAAAGGG 536
Db 421 ATCACTGCTTCTATTAGTTTGGTAGCGGTAGGAAATCGAATGCTTCCACGATAAAGGG 480
Qy 537 CACACTGGGATTTACTATATCGAATATCCGTATATGGCGTTTTTGGTATCATTCAA 596
Db 481 CACACTGGGATTTACTATATCGAATATTCCTGATATGGCGTTTTTGGCAATTTACG 540
Qy 597 GTTATTTCTTAGCCAGATCCCAATTTCCAAAGCTCTCTTTTCTTTCATTTATGCCGCA 656
Db 541 GTTATTTCTTAGCCAGATCCCAATTTCCAAAGCTCTCTTTTCTTTCATTTATGCCGCG 600
Qy 657 GTCATGTCCTTTACTTATGCACTATTGGAATCGGTCTAGCCATCGCAACCGTCGAGGT 716
Db 601 GTCATGTCCTTTACTTATGCACTATTGGAATCGGTCTAGCCATCGCAACCGTCGAGGT 660
Qy 717 GGGAAAGTGGTAAAGCAGTATGACGGGCAACGCGTGTGGAGTAGATGTAAACCGCAGCT 776
Db 661 GGGAAAGTGGTAAAGCAGTATGACGGGCAACGCGTGTGGAGTAGATGTAAACCGCAGCT 720
Qy 777 CAAGAATATGGAGATGTTTCAAGCGTTTGGGACATAGCTTCCGCTATGCTTATGCC 836
Db 721 CAAGAATATGGAGATGTTTCAAGCGTTTGGGACATAGCTTCCGCTATGCTTATGCC 780
Qy 837 ACGGTTCTCATCGAGATTCAGGATACACTAAGATCTAGCCAGCTTGAGAACAAAGCCATG 896
Db 781 ACGGTTCTCATCGAGATTCAGGATACACTAAGATCTAGCCAGCTTGAGAACAAAGCCATG 840
Qy 897 AABAAGCAAGCTTGTGGAGTATCAACACACCTTTTCTCATCTTATGTGGATGC 956
Db 841 AABAAGCAAGCTTGTGGAGTATCAACACACCTTTTCTCATCTTATGTGGATGC 900
Qy 957 ATCGGCTATGCTGCATTTGAAAACAATGCCCTCGGAGATTTCCCTCACAGATTTCCGGTTT 1016
Db 901 ATCGGCTATGCTGCATTTGAAAACAATGCCCTCGGAGATTTCCCTCACAGATTTCCGGTTT 960
Qy 1017 TTCAGGCCCTTTTGGCTCATTTGCAAGCTTTCATCGCTGCTCCACCTTATTTGGT 1076
Db 961 TTCAGGCCCTTTTGGCTCATTTGCAAGCTTTCATCGCTGCTCCACCTTATTTGGT 1020
Qy 1077 GCCTATCAGGTGTTCCGCGACGCGATTTCCAGTTTGTGAGAAAATAATCAACAGAAAC 1136
Db 1021 GCCTATCAGGTGTTCCGCGACGCGATTTCCAGTTTGTGAGAAAATAATCAACAGAAAC 1080
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Db 1141 TTCACATTAAGCCTTTTCAGATTTGGTGTGGAGACAGCTTATGTGGTTTAAACCACTGTT 1200
Qy 1257 GTAGCTATGATATTCCTTTCTTCAACGCGATCTTAGGTCTTATCGGAGCAGCTTCCTTC 1316
Db 1201 GTAGCTATGATATTCCTTTCTTCAACGCGATCTTAGGTCTTATCGGAGCAGCTTCCTTC 1260
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Qy 1317 TGGCCTTTAAACGGTTTATTTCCCTGTGGAGATGCATTTGCACAAACCAAGATTAAAG 1376
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Db 1321 TACTCTGCTAGATGGAATTCGCTGAAAACGATGTGCTATGTTTCTTGTGATCGCTC 1380
Qy 1437 TTAGCTGCAGCGGATCCATCGCAGGACTTATAAGTAGTGTCAAAACCTCAAGCCCTTC 1496
Db 1381 TTAGCTGCAGCGGATCCATCGCAGGACTTATAAGTAGTGTCAAAACCTCAAGCCCTTC 1440
Qy 1497 CGGACTATGCATGAGTGA 1514
Db 1441 CGGACTATGCATGAGTGA 1458

RESULT 2
US-09-938-842A-802
; Sequence 802, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 802
; LENGTH: 1446
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-802

Query Match 42.9%; Score 722.2; DB 9; Length 1446;
Best Local Similarity 71.1%; Pred. No. 6.1e-202;
Matches 984; Conservative 0; Mismatches 393; Indels 6; Gaps 2;

Qy 126 GACCCGACAAAGAACGTCGATGAAGATGTCGAGAGAGCGTACCGGAGCGTGGCTTACG 185
Db 58 GATACTAACAAAACCTTTTCGAGGATGGCCGACAAAAGAACTGGGACATGGATGACC 117
Qy 186 GCAGATGCGCATATATACGCGGTGATAGCTCCGGAGTGTGTCTTTAGCATGGCT 245
Db 118 GGGNGTGCACATATAACGGCCGTGATAGGTCGGAGTGTGTCTTTGGCGTGGCA 177
Qy 246 ATAGCTCAGCTTGGTGGATTCGAGGACATCGATCTTACTCATTTTCTGTTCACT 305
Db 178 ATCGCACAACTTGGATGGGTGGCAGGACCCGCGTACTTAATGGCTTTTCTTTCATAACA 237
Qy 306 TACTTTCACCTCCACCATGCTTCCGATTCCTACCGTGGCGGATCCCGTACCGGAAAA 365
Db 238 TATTTTACATCAACCATGCTTCCGATTTGTACCGTCCCTGACCTGTGTACCGGCAA 297
Qy 366 CGAATTTACATTTACATGACCGTTGTTCGATCTTACCTCGGTGTAGGAAAGTGCAGTC 425
Db 298 CGCACTACACCTTACATGGAAGTTGTCCGATCTTATCTAGGAGGAGAAAGTGCATTA 357
Qy 426 TGTGGAGTGGCAAAATATGGGAATCTGATTTGGGGTCACTGTGTGGTTACACCATCCTGCT 485
Db 358 TGTGGATTTGGTCAATACCGGATCTGATTTGGAATTAACAATCGCTACACATCAGACT 417
Qy 486 TCTATTAGTTTGGTAGCGGTAGGGAATCGAACTGCTTCCACGATAAAGGCGACACTGGG 545
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Db 418 TCAATAGCATGCTGGCAGATGAGAGGTGCAATTTGTTCCACAAAAAGGGCATATCTT 477  
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Db 478 AATGTGCACTTAAACACTCCCTTCATGATCAATTTGCAATCATCAATTAATTTCTT 537  
Qy 606 AGCCAGATCCCAATTTCCACAAGCTCTCTTTCTTCCATATGAGCGGAGTCATGTC 665  
Db 538 AGCCAAATCCCAATTTCCAAATCTCTCTGCTCTCATTTCTTGCGCGTAAATGTC 597  
Qy 666 TTTACTATGCACTATGGAATCGGTTAGCCATGCAACCGTCGAGGTGGAAAGTG 725  
Db 598 TTTTGTATGCTTCACATGGGTGTGCTCTCATGCGCAAGCGCGGTGGCGGTAG 657  
Qy 726 ---GGTAAAGCATATGACGGGACAGCGGTGAGTATGATTAACGAGCTCAAAAG 782  
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Qy 783 ATATGAGATGTTTCAAGCGGTTGGGACATAGCCTTGCTATGCTTATGCCAGGTT 842  
Db 718 ATATGAGAAAGTTCACAGGATGAGGACATTTGCTTACGATCTCAATCTGTT 777  
Qy 843 CTCAATGAGATTCAGATATACATTAAGTTC---TAGCCAGCTGAGAAAGCCATGAA 899  
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Qy 900 AGAGCAAGCTTTGGGAGATATCAACACACTTTTTCATCATCTATGTGATGATC 959  
Db 838 AGAGCAAGCTTTGGGAGTCTCCACAAACCTCTCTCAATATTTAGCGGTGTG 897  
Qy 960 GGTATGCTGATTTGGAACAAATGCCCTGAGATTTCTCTCAAGATTTGGGTTTTC 1019  
Db 898 GGTATGCTGCTTTGGAATGATGCTCCGAAATTTCTCAAGTGTGTTGTTCTAT 957  
Qy 1020 GAGGCTTTTGGCTCATTTGACTTTGCAAGCTTGATGCTGCTCACTTATTTGGTCC 1079  
Db 958 GAGGCTTTTGGCTCATTTGACTTTGCAAGCTTGATGCTGCTCACTTATTTGGTCC 1017  
Qy 1080 TATCAGGTGTCGCGACGCGATATTCAGTTGTTGAAAAAAATGCAACAGAACTAT 1139  
Db 1018 TACCAAGCTTTTTCACAAATTTTTCAGTTGTTGAGAGGACGAGCGGAAAGTTGG 1077  
Qy 1140 CCAAGCAAGATTCATCATCTTGAATTTAGTAAAGTATCTTTCTTGGAAATTC 1199  
Db 1078 CCGATTAACAAGTTATTTACAGAGATTAACAATTCATGTCCTTGTGCTGTGATTTT 1137  
Qy 1200 AACATTAGCTCTTCAGATGTTGTGAGAGACGTTATGAGTTAAACCATGTTGA 1259  
Db 1138 AGTATCAACTCTTCAGATGTTGTGAGAGACGTTATGTTGTGTTCAACGCGGTTGA 1197  
Qy 1260 GCTATGATATTCCTTTCTTCAAGCGATTTAGTCTTATGAGAGCTTCTCTTGG 1319  
Db 1198 GCGATGATCTTCTTCTTCTTCAAGATTTCTTGTGCTTATTTGAGAGCTTCTCTTGG 1257  
Qy 1320 CTTTAAAGCTTTATTTCCCTGTGAGAGATGACATGCAACAAACGATTAAGAAAGTAC 1379  
Db 1258 CTTTGAAGCTTTATTTCTTCAATTTGATGATGATTTGCTCAAGAGAGTACCGAAATTC 1317  
Qy 1380 TCTGCTAGATGATGCTGCTGAAGAAAGATGCTATGTTGCTTATGCTCTGCTTGA 1439  
Db 1318 TCTTTCATCTTGGACTTGGTTAAATTTCTGATTTGATGATTTCTTCTTCTTCTT 1377  
Qy 1440 GCTGAGCGGATCCATGCGAGCATTAATAGTGTCAAAACCTACAAAGCCCTTCCGG 1499  
Db 1378 GCTGAGCGGATCAGTGAAGAGATCATCAAAAGTCTCAAGATTTCAAGCTTCTCAG 1437  
Qy 1500 ACT 1502  
Db 1438 GCT 1440

RESULT 3

US-09-938-842A-67  
; Sequence 67, Application US/09938842A  
; Patent No. US20020160378A1  
; GENERAL INFORMATION:  
; APPLICANT: Harper, Jeff  
; APPLICANT: Kreps, Joel  
; APPLICANT: Wang, Xun  
; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
; TITLE OF INVENTION: SAME, AND METHODS OF USE  
; FILE REFERENCE: SRIPI300-3  
; CURRENT APPLICATION NUMBER: US/09/938,842A  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: US 60/227,866  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/264,647  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/300,111  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 5379  
; SEQ ID NO 67  
; LENGTH: 1431  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-938-842A-67  
  
Query Match 30.1%; Score 507.2; DB 9; Length 1431;  
Best Local Similarity 61.2%; Pred. No. 8,4e-138;  
Matches 837; Conservative 0; Mismatches 528; Indels 3; Gaps 1;  
  
Qy 123 CAAAGAACGTGATGAGATGCTGAGAGAGAGCGTACCGGAGCGTGGCTTACCGGAGATG 192  
Db 56 CCAAGTACTTGGAGAGAGAGCGGMAAAACAAAGAACTGGAGTGTGGACGCGAGATG 115  
Qy 193 GCGATATTTACCGCGGTATAGCTCCGAGTGTGCTTTAGCATGGGTATAGCTC 252  
Db 116 CACACATATTAACGCGAGTATAGTTCGGAGTTTGTCTACAGTGGGTACGGGCGC 175  
Qy 253 AGCTTGTGATGAGAGAGACATCATCTTACTCATTTTCTGTTCAATTTACTTCA 312  
Db 176 AGCTATGTGCTCGCGGACCGGTGTATGTTGCTTCTCTGCGCTCACTTATTTCA 235  
Qy 313 CCTCACCATGCTTGGCGATTTGCTACCGTGGCGGATCCGTCACCGGAAACGGAAT 372  
Db 236 CTTCTTCTTCTTGTGCTGTGTTACCGCTCGGCAACCTATTCGCGCAAGAACT 295  
Qy 373 AACTTACATGAGCGTGTGATCTTACTCTGCTGTGAGAAAGTGCAGCTCTGTGAG 432  
Db 296 AACTTATATGATGCTGCTCCATCAATCTGCTGCGCTGAAGTGAAGCTATGTGGA 355  
Qy 433 TGGCAATATGGAATCTGATTTGGGCTCACTGTGTTACATCACTACTGCTTTATTA 492  
Db 356 TTGTTCAATATCTTAATCTTGTGTGTGCTATTGTGCTACCAATTTGCTTACGTATA 415  
Qy 493 GTTGTGCGGTGAGGAATGCAACTGCTTCACGATTAAGGCACTGCGGATTTGA 552  
Db 416 GATGATGGAATTAAGATCAAACTGTTCCACAAGATGGAAGGAAGATTCATGTC 475  
Qy 553 CTATATCGAATTAATCGATATGAGCGGTTTGGTATCACTCAAGTATTTCTTACCGA 612  
Db 476 AACTTAACAGTAATCTTACATGATGCTTTGATTAATGATTCAGATTTCTCTCA 535  
Qy 613 TCCAAATTTCCAAAGCTCTCTTTCTTCAATTTAGCGCCAGTATGCTTACTT 672  
Db 536 TTTCAATTTTGAATCACTTTGAGTGTCTCAATCTCGCGCGGTATGTCCTTCACTT 595  
Qy 673 ATGCACTATTGGAATGGCTTACCATGCAACCGTCCAGGTGGAAGTGGTAAAG 732  
Db 596 ATTCCTGAGCGGTCTCGCCTCGGCAATGCCCAATTTGTGTATATGGAAGTGAAG 655  
Qy 733 CGAGTATGAGCGGACAGCGGTGAGTATGATTAACCCAGCTCAAAAGATATGAGAT 792  
Db 656 GAAATCTCACTGGGATTTAGCATAGAGCA---GTAAAGAGACACAGAAAGATATGAGGA 712

Qy 793 CGTTTCAAGCGTTGGGACATAGCGTTCCGCTTATGCTTATGCCACGGTTCTCATCGAGA 852  
Db |||||  
Qy 713 CTTTCAAGCTCTTGGAGACATGCTTTTGTCTTACTCTTACTCCATTATCTCTCATCGAGA 772  
Db |||||  
Qy 853 TTCAGGATACATTAAGATCTAGCCAGCTGAGAACAAAGCCATGAAAGAGCAAGTCTTG 912  
Db |||||  
Qy 773 TTCAGGACACAGTCAAGTCAACCATCAGAGAGAGACGATGAAGAAGCAACACTTG 832  
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Qy 913 TGGAGATATCAACACACACTTTTCTACATCTATATGAGATGATCGGCTATGCTGCAT 972  
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Qy 833 TGACGCTCAGTGAACGACTATCTTCTATATGTTGTGTGATATGAGGATATGACGCT 892  
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Qy 973 TTGAAACAATGCCCTCGGAGATTTCTCACAAGATTCGGGTTTTTCAGGCCCTTTTGGC 1032  
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Qy 1033 TCATGACTTTGCAAGCTTTGATCGCTGTCCACTTATTTGGTGCCTATCAGGTGTTG 1092  
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Db |||||  
Qy 1073 TCATTTGCAAGAGATATCAAAATTCCTGTTTCAAGCTCTCGGCTTGAATGTCT 1132  
Db |||||  
Qy 1213 TCAGATTTGGTGTGGAGACAGCTTATGTGTTTAAACACTGTTGTAGCTATGATATTC 1272  
Db |||||  
Qy 1133 TCAGTTGATATGGAGACAGTGTGTTGATCATACGACAGTATCTCAATGCTTCTTC 1192  
Db |||||  
Qy 1273 CTTTCTCAAGCGGATCTTAGTCTTATCGGAGAGCTCTCTTCTGGCTTTTAACGGTTT 1332  
Db |||||  
Qy 1193 CGTTTTCAGAGCTTGTGGGCTCTGCTCGGGGCACTAGGGTTTTTGGCCATTGACGGTGT 1252  
Db |||||  
Qy 1333 ATTTCCCTGTGGAGATGCATTTGCAAAACCAAGATTAAAGTACTCTCTAGATGGA 1392  
Db |||||  
Qy 1253 ATTTTCAGTGGAAATGTACATCGCAGAGAGATACCTAGATGGAGCACAGATGG 1312  
Db |||||  
Qy 1393 TTGGCTGAAAAAGATGCTATGTTGTTGATGCTGCTGCTTGTAGCTGACCGCGAT 1452  
Db |||||  
Qy 1313 TTTGCCCTTCAAGTCTTCAAGCTTAGGCTGTCTAGTAGTTAGCATTTGCTGACGCTGACGGGT 1372  
Db |||||  
Qy 1453 CCATCGCAGGACTTATAAGTAGTGTCAAAACCTACAGGCCCTTCGGA 1500  
Db |||||  
Qy 1373 CCATAGCTGGAGTACTTCTTGAATCTAAGTCTTACAGCCATTTCGAA 1420  
Db |||||

## RESULT 4

US-09-938-842A-1482  
; Sequence 1482, Application US/09938842A  
; Patent No. US20020160378A1  
; GENERAL INFORMATION:  
; APPLICANT: Harper, Jeff  
; APPLICANT: Kreps, Joel  
; APPLICANT: Wang, Xun  
; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
; TITLE OF INVENTION: SAME, AND METHODS OF USE  
; FILE REFERENCE: SCRI1300-3  
; CURRENT APPLICATION NUMBER: US/09/938,842A  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: US 60/227,866  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/264,647  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/300,111  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 5379  
; SEQ ID NO 1482  
; LENGTH: 1482

TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-938-842A-1482

Query Match 29.8%; Score 501.8; DB 9; Length 1482;  
Best Local Similarity 61.3%; Pred. No. 3.3e-137;  
Matches 844; Conservative 0; Mismatches 527; Indels 6; Gaps 2;

Qy 135 AAGAACCTGCATCAAGATCGTCGAGAGAGCGTACCAGGAGCTGGCTTACGGGAGTGGC 194  
Db |||||  
Qy 106 AATGCTTCGATGATGCGCGCTCAAAAGAACTGGGACTGTTTGGACCGGAGCGCT 165  
Db |||||  
Qy 195 CATATTATACCGCGCGTGTAGGCTCCGAGGTGTTGCTTTAGCATGGGTATAGTCTCAG 254  
Db |||||  
Qy 166 CATATAATAACTCGCGTTATCGGATCCGCGGTTTTGTCATTTGGCGTGGCGGATTCACAG 225  
Db |||||  
Qy 255 CTGGTTGGATCCGAGGACATCGATCTTACTCATTTCTCGTTCATTACTTACTCACC 314  
Db |||||  
Qy 226 CTGCGATGGATCTCGGCCCTCTGTGATGTTATTTCTCTCTCTTTACTTCTTACTCC 285  
Db |||||  
Qy 315 TCCACCATGCTTCCCGGATTCGCTACCGTCCGCGGATCCCGTCAACGGAACCGGAATTAC 374  
Db |||||  
Qy 286 TCCACACTTCTTAGCGACTGTCTACAGAACCGCGGATGCAAGTCTGCGCAAGAGAACTAC 345  
Db |||||  
Qy 375 ACTTACATGACGCTTGTTCGATCTTACTCTCGTGTGAGAAAGTGCAGCTCTGTGGAGTG 434  
Db |||||  
Qy 346 ACTTACATGATGCGGCTTCGATCAATTTCTCGGTGGGTTCAAGTTTCAAGATTTGTGGGTG 405  
Db |||||  
Qy 435 GCACAATATGGGAATCTGATTTGGGCTCACTGTTGGTTACACCATCACTGCTTCTATTAGT 494  
Db |||||  
Qy 406 ATTCAATACTTGAATCTCTTTGGTATCGCAATTTGATACACGATAGCAGCTTCCATAAGC 465  
Db |||||  
Qy 495 TTGTAGCGGTAGGGAATCGAATGCTTCCACGATAAGGGCACACTGGGGATTGACT 554  
Db |||||  
Qy 466 ATGATGCGATCAAGAGATCCAACTGCTTCCACAGAGTGGAGAAAGAACCCATGTGAC 525  
Db |||||  
Qy 555 ATATCGAATTTATCCGTATATGGCGTTTTTGGTATCATTTCAAGTTTATTTCTTAGCCAGATC 614  
Db |||||  
Qy 526 ATGTCCAGTAATCTTTACATGATCGTATTTGGTGTGGCAGAGATCTTGCTCTCTCAGTT 585  
Db |||||  
Qy 615 CCAATTTTCCAAAGCTCTCTTTTCTTCCATTATGGCGCAGTCATGCTCTTACTTAT 674  
Db |||||  
Qy 586 CCGTATTTGATCAGATTTGGTGGATCTCCATTTGTGAGCTGTTATGTCTTCTACCTTAC 645  
Db |||||  
Qy 675 GCAACTATTGGAACTCGGCTAGCCATCGCAACCGTCCGAGTGGGAAAGTGGGTAAAGACG 734  
Db |||||  
Qy 646 TCTGCCATTGCTAGCTCTTGGAACTCGTTCAAGTTGCGAGCGAATGGAGTTTTCAAAGGA 705  
Db |||||  
Qy 735 AGTATGACGGGACACGGGTTGGAGTAGATGTAACCGAGCTCAAAAGATATGAGATCG 794  
Db |||||  
Qy 706 AGTCTCACTGGAATAGCATCGGAACA---GTGACTCAAAACACAGAAAGATATGGAGAAC 762  
Db |||||  
Qy 795 TTTCAAGCGGTTGGGACATAGCTTTCGCTTATGCTTATGCGCGTTCTCATCGAGATT 854  
Db |||||  
Qy 763 TTCCAAGCACTGGAGACATTTGCCCTTGGGTACTCATACTCTGTTGCTTCTTANTCGAGATT 822  
Db |||||  
Qy 855 CAGGATACATAAGTCTAGCCAGCTGAGAACAAAGCCATGAAAGAGCAAGTCTTTGTG 914  
Db |||||  
Qy 823 CAGGATCTGTAAAGTCCCCACCGCGGAATCGAAACGATGAAAGAAAGCAACAAAATC 882  
Db |||||  
Qy 915 GGAGTATCAACCACTACTTTTCTTACATCTTATGTGATGATCGCTGCTGCTCAATGGGTAT 974  
Db |||||  
Qy 883 AGTATTCGCTGACACTATCTTTACATGCTATGCTGCTCAATGGGTATATGCGCTTTT 942  
Db |||||  
Qy 975 GGAACAATGCCCTCGAGATTTCTCTCAGATTTCCGGTTTTTCGAGGCCCTTTGGCTC 1034  
Db |||||  
Qy 943 GGAGATGCAACACCGGAAACCTCTCTACCGGTTTTTGGATTTCTACAACCCGTTTTGGCTC 1002  
Db |||||  
Qy 1035 ATTGACTTTGCAAAACGCTTGCATCGCTGTCCACCTTATTGTGTGCTTATCAGGTGTTGCG 1094  
Db |||||  
Qy 1003 CTTGACATAGCTAAAGCGCGCAATTTGTTCCACCTCGTTGGAGCTTTACCAAGTCTTTGCT 1062  
Db |||||  
Qy 1095 CAGCCGATATTCAGTTTCTTGAGAAAAATGCAACAGAAACTATCCAGACACCAAGTTC 1154  
Db |||||





QY	1197	TTCAACATAGACCTCTTCAAGTTTGGTGGAGACAGCTTATGTGGTTATTAACAACGTGT	1256
Db	446	TACAAGTCACAGTTTTCAGACAGTTTACCAACGGGTTTGTGGTTTGAACACATGG	387
QY	1257	GTAGCTATGATATTCCTCTTCTTCAACGGCATCTTAGCTCTTATCGACAGCCTTCCTTC	1318
Db	386	AATATCATGCTTATGCGGTATTTCAACGACGCTGATAGGAACTTATAGTGTGGTAGGGTT	327
QY	1317	TGGCCTTTAAGCGTTTATTTTCCGTGTGAGATGCACTTGGACAAACCAAGATTAGAAG	1376
Db	326	TGGCCTTTGAACGGTTTACTTTCCGGTGGAGATGTATATAGACAGAGAAAGTTTACAGA	267
QY	1377	TACTGTCTAATGGATTGGCGCTGAAAACGATGTGCTATGTTTGCTGATCGTCTGCTC	1438
Db	266	TGGAGATCAAGATGGGTTGTCTGCAGATGTTAGCTGGGTGTTGAATGAATCAAGTTG	207
QY	1437	TTAGCTGACGCCGATCATCGACAGACTTATTAAGTAGTGTCAAAACCTTCAAGCCCTTC	1498
Db	206	GTGCGCGGAGTTGGCTCCATGCGCGAGTAATGTAGACCTTAAGTTTCAAGCCGTTTC	147
QY	1497	CGGACTA	1503
Db	146	AAGACTA	140

```

RESULT 10
US-09-878-574-103
Sequence 103, Application US/09878574
Patent No. US20020110548A1
GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ. ID NOS: 15775
SEQ. ID NO 103
LENGTH: 383
TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: LIE3028-056-01-B1-B2
US-09-878-574-103

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	Query Match	Score	DB	Length
	100.0%	10.4	10	383
	Best Local Similarity	60.2%	Pred. NO. 5.6e-20	
	Matches	169	Conservative	0
			Mismatches	111
			Indels	0
			Gaps	0
Qy	131	GACAAAGACCTGCATGAAGATGTCGAGAGAAGCGTACCGGGACGTGGCTTACCGGCGAG	190	
Dh	87	GTCGAAATTCCTACGATGATGATGGTCATGTTAAAGGAAACAGGGAACGTTTGGATCAAG	146	
Qy	191	TGGCATATTATACAGCGCGGTGAATGAGCTCCGAGAGTGTGTTTGTAGCATGGGTATAGC	250	
Dh	147	CTGGCAATATATAACAGCAAGATGGTGGGTTCTGGGGTGTGTCTTTGGCATGGGCAATGGC	206	
Qy	251	TCAGCTTGTTGATGCGAGGAGACATGATCTTACTCATTTTCTCGTTCACTTACTTACTT	310	
Dh	207	TCAATGGGTGGGTGTGCTGGGCTGTGATGTTGATCTTCTTCACGTGCTGTATGAGTTGA	266	
Qy	311	CACCTCACCATGCTTCCGATGCTTACCGTGGCGCGGATCCCGTCAACCGGAAACGGAA	370	
Dh	267	TACAGACGTCCTCTGCTCATATTGTTATTCGGTGCAGTACCCCGTTACGGGGAAGAGAA	326	
Qy	371	TTACACTTACATGAGCGTTTTCGATCTTACTCTGGTGG	409	
Dh	327	CTATACCTTTCATGATGACATTTCAATTCATTTCTGGCGG	365	

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11 RESULT 11
12 US-09-878-574-5991
13 ; Sequence 5991, Application US/09878574
14 ; Patent No. US20020110548A1
15 ; GENERAL INFORMATION:
16 ; APPLICANT: Byrum, Joseph R.
17 ; APPLICANT: La Rosa, Thomas J.
18 ; APPLICANT: Thompson, Michael D.
19 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
20 ; TITLE OF INVENTION: Plants
21 ; FILE REFERENCE: 38-21 (15401) B
22 ; CURRENT APPLICATION NUMBER: US/09/878,574
23 ; CURRENT FILING DATE: 2001-12-21
24 ; PRIOR APPLICATION NUMBER: 09/333,535
25 ; PRIOR FILING DATE: 1999-06-14
26 ; NUMBER OF SEQ. ID NOS: 15775
27 ; SEQ. ID NO 5991
28 ; LENGTH: 264
29 ; TYPE: DNA
30 ; ORGANISM: Glycine max
31 ; OTHER INFORMATION: Clone ID: 701097612H1
32 US-09-878-574-5991

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	Query Match	Score	DB	Length
Best Local Similarity	60.5%	Pred. No. 5.1e-18		264;
Matches	155;	Conservative	0;	Mismatches 101; Indels 0; Gaps
QY	1140	CCAGACACAACTTCATCTACTCTGTAATTCAGTAAACGTAACCTTCCCTGGAAATTC	1199	
Db	7	CCATAATAGATTTTATATGACAGAGAGTTGAAGTACCAATCCCTGGTTGCAAAACCTTAC	66	
QY	1200	AACATTAGCCTCTTCAGATTGATGTGAGAGAGAGCTTATGTGTTATTAACACTGTGTTA	1253	
Db	67	AACCTAACCTCTTCAGTTAGTTGGATTTGGAGACACTTTTGTGATTTTGTCAACTGTGATA	126	
QY	1260	GCATATATATTTCCCTTTCTTCAACGGATCTTAGGTTCTTAATCGAGAGAGTTCTCTTCG	1319	
Db	127	GCATCTCTCTTACCAATTTCTTCAATGACATTGATCCGTTATTTGAGCCATGTGATTTGG	186	
QY	1320	CCTTTACACGTTTATTTTCCCTGTGAGATGACATTTGACAAACCAAGATTAAAGAGTAC	1379	
Db	187	CCCCACATGTTATTTTACGATGGAGATGTATATTAACCTAACTAAGATACCAAGTGG	246	
QY	1380	TCTGTCAATGATGATTG	1395	
Db	247	GGCATAAATGGATTG	262	

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RESULT 12
US-09-878-574-3794
/ Sequence: 3794, Application US/09878574
/ Patent No. US20020110548A1
/ GENERAL INFORMATION:
/ APPLICANT: Byrum, Joseph R.
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Thompson, Michael D.
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
/ TITLE OF INVENTION: Placens
/ FILE REFERENCE: 38-21 (15401) B
/ CURRENT APPLICATION NUMBER: US/09/878,574
/ CURRENT FILING DATE: 2001-12-21
/ PRIOR APPLICATION NUMBER: 09/333,535
/ PRIOR FILING DATE: 1999-06-14
/ NUMBER OF SEQ ID NOS: 15775
/ SEQ ID NO 3794
/ LENGTH: 386
/ TYPE: DNA
/ ORGANISM: Glycine max
/ OTHER INFORMATION: Clone ID: LIB3028-005-Q1-B1-G8
US-09-878-574-3794

```

Query Match 5.2%; Score 88.2; DB 10; Length 386;

Best Local Similarity 58.0%; Pred. No. 4.2e-16;  
Matches 156; Conservative 0; Mismatches 113; Indels 0; Gaps 0;

Qy 111 GCCTACACCGTGTGGACCGGACAAAGAAAGCTCGATGAAGATGGTCGAGAGAAAGCTACC 170  
Db 117 GACAAACCAAGCCCTTATCGAACTGGAACCTCGACGATGGCGAGAAATCAGAAGAAC 176  
Qy 171 GGGACGTGGCTTACGGGAGTGGCGATATATACAGCGCGGTGATAGGCTCCGGAGTGTG 230  
Db 177 GGGAAATGTGTGGACTGTAAACATACATATTAACAGTGGTGTAGGGGCGAGGGGTGCTG 236  
Qy 231 TCTTAGCATGGGTATAGCTAGCTAGCTGGTGGTGGATCGCAGGAGACATCAATCTTACTCATT 290  
Db 237 TCTTTGGCATGGGTATGGCACAACCTAGGATGGTGGATAGCCAGATCATTTACC 296  
Qy 291 TTCTCGTTCACTTACTTACCTACCTACCATGCTTCCGATGCTACCGTGGCCCGGAT 350  
Db 297 TTTTCAGCTGTGCGCAATTTTCACCTTCAATCTTGTAGCTGATTTACAGATATCCAGAC 356  
Qy 351 CCCGTACCGGAAACCGAATTACACTTA 379  
Db 357 CCTGTCACTGGCAGAGAAATTTACTTA 385

RESULT 13  
US-09-878-574-1977  
; Sequence 1977, Application US/09878574  
; Patent No. US20020110548A1  
; GENERAL INFORMATION:  
; APPLICANT: Byrum, Joseph R.  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Thompson, Michael D.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(15401)B  
; CURRENT APPLICATION NUMBER: US/09/878,574  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 09/333,535  
; PRIOR FILING DATE: 1999-06-14  
; NUMBER OF SEQ ID NOS: 15775  
; SEQ ID NO 1977  
; LENGTH: 307  
; TYPE: DNA  
; ORGANISM: Glycine max  
; OTHER INFORMATION: Clone ID: LIB3028-030-Q1-B1-P3  
US-09-878-574-1977

Query Match 5.2%; Score 88; DB 10; Length 307;  
Best Local Similarity 55.6%; Pred. No. 4.2e-16;  
Matches 169; Conservative 0; Mismatches 135; Indels 0; Gaps 0;

Qy 374 CACTTACATGGACGCTTGTTCGATCTTACCTCGGTGGTAGAAAGTGCAGCTCTCTGGAGT 433  
Db 1 CTCCTACATGGATGCTGTAGATTTATCTTGGTTATAAAGGACATGTGTAGCTGCTT 60  
Qy 434 GGCACATATGGGAATCTGATTCGGGTCACTGTGGTACACCATCACTGCTCTATTAG 493  
Db 61 CTTTCAATTTTGTACTTTGTATGGTACTAGTATGCTTATGCTTAAACACAGCAACTAG 120  
Qy 494 TTTGGTAGCGGTAGGAAATCGAACTGCTTCCACGATAAAGGGACACCTGGGGATTGTAC 553  
Db 121 TCTGAGTGAATCTTGAGATCAATTTGTTATCACAAGAAAGGCGATGAAGCTCTCTGTA 180  
Qy 554 TATATCAATATTCGGTATATGCGGTTTTTGGTATCATCTCAAGTATCTTACCCAGAT 613  
Db 181 ATATGGTGGCAATCTGTATATGCACTGTTTGGACTGTGTTCAAGTGTGAATGTCAATCAT 240  
Qy 614 CCCAAATTTCCACAAGCTCTCTTTCTTTCCATTATGGCCGAGTCATGTCCTTTACTTA 673  
Db 241 ACCGGATCTCCATAACATGCGATGGGTTTCAGTTGTTGCAGCACTATGTCCTTTACATA 300  
Qy 674 TGCA 677

Db 301 CTCA 304

## RESULT 14

US-09-923-876-317  
; Sequence 317, Application US/09923876  
; Patent No. US20020013958A1  
; GENERAL INFORMATION:  
; APPLICANT: Lalgudi, Raghunath V.  
; APPLICANT: Kamigaki, Laura Y. (Ito)  
; APPLICANT: Sherman, Bradley K.  
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING  
; FILE REFERENCE: PL-0012-1 CON  
; CURRENT APPLICATION NUMBER: US/09/923,876  
; CURRENT FILING DATE: 2001-08-06  
; PRIOR APPLICATION NUMBER: 09/298,329  
; PRIOR FILING DATE: 1999-04-21  
; PRIOR APPLICATION NUMBER: 60/085,331  
; PRIOR FILING DATE: 1998-05-05  
; NUMBER OF SEQ ID NOS: 6332  
; SOFTWARE: PERL Program  
; SEQ ID NO 317  
; LENGTH: 238  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20020013958A1 700156744H1  
; NAME/KEY: unsure  
; LOCATION: 88, 92, 96  
; OTHER INFORMATION: a, t, c, g, or other  
US-09-923-876-317

Query Match 4.7%; Score 80; DB 10; Length 238;  
Best Local Similarity 61.2%; Pred. No. 8e-14;  
Matches 145; Conservative 0; Mismatches 88; Indels 4; Gaps 1;

Qy 328 CCGATTCTCTACCGTGGCGGATCCGTCACCGGAAACGGAATTACACTTACATGACG 387  
Db 1 CCGACTGCTTACCGACCGCCGACCCGCTCCAGGCGAAGGAAACCGCACTTACATGACG 60  
Qy 388 TTGTTGATCTTACCTCGGTGTGTAGAAAGTGCAGCT---CTGTGGAGTGGCACAATAT 443  
Db 61 TCGTCCGCTCATGCTCGGGCCTAGAGNTTGTGNTGTTGTTGGGACTCGCACAGTAC 120  
Qy 444 GGGAACTGTGATGGGTCACTGTGTTACACCATCACTGCTTCTATTAGTTGGTAGCG 503  
Db 121 GCGATCTCTGGGGGACAATGTGGCTACACCATCACTGCCACGACATCATGGCC 180  
Qy 504 GTAGGAAATCGAACTGCTTCCAGATAAAGGGCACACTGCGGATTTGCTATATATCG 560  
Db 181 GTGCGCGCACGACGACTGCCGCCACACACAGGCGGCCACGACGCGGCTCGGCTCGTGG 237

## RESULT 15

US-09-878-574-3185  
; Sequence 3185, Application US/09878574  
; Patent No. US20020110548A1  
; GENERAL INFORMATION:  
; APPLICANT: Byrum, Joseph R.  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Thompson, Michael D.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(15401)B  
; CURRENT APPLICATION NUMBER: US/09/878,574  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 09/333,535  
; PRIOR FILING DATE: 1999-06-14  
; NUMBER OF SEQ ID NOS: 15775  
; SEQ ID NO 3185  
; LENGTH: 382  
; TYPE: DNA



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; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-014-Q1-B1-P5
US-09-878-574-3185

Query Match      3.4%; Score 56.8; DB 10; Length 382;
Best Local Similarity 59.1%; Pred. No. 7e-07;
Matches 97; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

OY 144 GATGAAGATGGTCGAGAGAGCGGTACCGGAGCGTGGCTTAACGCGAGGTGGCGATATTATC 203
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 217 GATGATGATGACATGCCAAGAGACTGGGAATTTCAGAGTGTCTGTAGCTCATATTCATT 276
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 204 ACGGCGGTGATAGGCTCCGAGGTGTGTCTTTAGCAATGGGCTATAGCTCAAGCTTGTTGG 263
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 277 ACTGCTGTATTGGTCTGGGTCTTCTTCTTCCTTGCAATGGAGCACTTCCCAATTAGGATGG 336
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 264 ATCGAGGAGACATGATCTTACTCATTTTCTGCTCATTA 307
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 337 ATTGAGGAGCCATTTCCTTCTTGTGTCATTTGCACCTA 380
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Search completed: December 1, 2002, 10:32:14  
Job time : 78 secs



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: December 1, 2002, 08:56:52 / Search time 2037 Seconds  
(without alignments)  
13396.856 Million cell updates/sec

Title: US-09-854-562-1

Perfect score: 1685  
Sequence: 1 CTTAAAAACATTATTTTATC.....TTCCAAAAA..... 1685

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 1615406 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

EST: \*  
1: em\_estba: \*  
2: em\_esthum: \*  
3: em\_estlin: \*  
4: em\_estnu: \*  
5: em\_estov: \*  
6: em\_estpl: \*  
7: em\_estro: \*  
8: em\_hic: \*  
9: gb\_est1: \*  
10: gb\_est2: \*  
11: gb\_hic: \*  
12: gb\_est3: \*  
13: gb\_est4: \*  
14: gb\_est5: \*  
15: em\_estfun: \*  
16: em\_estom: \*  
17: gb\_gss: \*  
18: em\_gss\_hum: \*  
19: em\_gss\_iny: \*  
20: em\_gss\_pln: \*  
21: em\_gss\_vic: \*  
22: em\_gss\_fun: \*  
23: em\_gss\_mam: \*  
24: em\_gss\_mus: \*  
25: em\_gss\_other: \*  
26: em\_gss\_pro: \*  
27: em\_gss\_rtd: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	578.4	34.3	614	10	AV826998
2	473.8	28.1	545	9	AV826998
3	434	25.8	434	10	AV796991
4	416.4	24.7	418	10	AV804261
5	415	24.6	415	10	AV803440
6	411.4	24.4	414	10	AV803032

C	7	409.4	24.3	411	10	AV820846	AV820846
C	8	407	24.2	407	10	AV815645	AV815645
C	9	404.8	24.0	421	10	AV810513	AV810513
C	10	402	23.9	419	10	AV818296	AV818296
C	11	396	23.5	408	10	AV814816	AV814816
C	12	394.8	23.4	405	10	AV812283	AV812283
C	13	391	23.2	391	10	AV802054	AV802054
C	14	389	23.1	401	10	AV800991	AV800991
C	15	386.6	22.9	405	10	AV802975	AV802975
C	16	378.8	22.1	803	12	BC588608	BC588608
C	17	368.4	21.9	1756	11	AV109232	AV109232
C	18	363.4	19.8	667	9	A0237594	A0237594
C	19	312	18.5	3157	17	AB030808	AB030808
C	20	300.6	17.8	654	10	AW560155	AW560155
C	21	288	17.1	603	13	BI096983	BI096983
C	22	287.4	17.1	617	14	BO850879	BO850879
C	23	283.4	16.8	825	10	BE040834	BE040834
C	24	273.2	16.2	741	12	BE999727	BE999727
C	25	272.2	16.2	726	14	BU023358	BU023358
C	26	267.2	15.9	560	10	AW203255	AW203255
C	27	265.8	15.8	592	10	AW737124	AW737124
C	28	265.4	15.7	390	12	Z18061	Z18061
C	29	264.8	15.7	676	12	BC449684	BC449684
C	30	260.4	15.5	619	10	AW586710	AW586710
C	31	259	15.4	718	14	BO165802	BO165802
C	32	259	15.4	720	17	BH525612	BH525612
C	33	259	15.4	777	12	BC582749	BC582749
C	34	258.4	15.3	582	12	BF423871	BF423871
C	35	252.6	15.0	614	13	BU277500	BU277500
C	36	250.6	14.9	721	14	BO856263	BO856263
C	37	250.4	14.9	701	14	BO857040	BO857040
C	38	250.2	14.8	569	13	BI698982	BI698982
C	39	250	14.8	551	13	BM521152	BM521152
C	40	247.6	14.7	700	9	AL505065	AL505065
C	41	246.8	14.6	561	13	BM526380	BM526380
C	42	246.8	14.6	571	10	AV440612	AV440612
C	43	245.8	14.6	546	14	BO453973	BO453973
C	44	244.2	14.5	686	12	BF634717	BF634717
C	45	243.8	14.5	692	14	BO762905	BO762905

## ALIGNMENTS

RESULT 1  
LOCUS AV826998 614 bp mRNA linear EST 01-APR-2002  
DEFINITION AV826998 RAF19 Arabidopsis thaliana cDNA clone RAF109-10-F18 5',  
mRNA sequence.  
ACCESSION AV826998  
VERSION AV826998.1 GI:19869058  
KEYWORDS EST.

## ORGANISM

thale cress.  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidops.

## REFERENCE

1 (bases 1 to 614)  
Seki, M., Natsuka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,  
Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,  
Arai, K., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.  
and Shinozaki, K.

## TITLE

## JOURNAL

## COMMENT

Large scale analysis of Arabidopsis full-length cDNA (2002b)  
Unpublished (2002)  
Contact: Motoaki Seki  
Plant Functional Genomics Research Group  
RIKEN Genomic Sciences Center  
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
Tel: 81-298-36-4359  
Fax: 81-298-36-9060  
Email: msekic@riken.go.jp  
An Arabidopsis full-length cDNA library was constructed essentially  
as reported previously (Seki et al., 1998). cDNA cleaved with BamHI

and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pBluescript vector. Please visit our web site ([http://www.gsc.riken.go.jp/e/plant/index\\_e.html](http://www.gsc.riken.go.jp/e/plant/index_e.html)) for further details.

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		/db_xref="taxon:3702"
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		/clone_lib="RAF49"
		/dev_stage="plants at various developmental stages from germination to mature seeds"
		/lab_host="DH10B"
		/note="Site 1: BamHI; Site 2: SalI; subjected to dehydration(1, 2, 5, 10, 24 hr) treatments"
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	Best Local Similarity	99.5%; Pred. No. 3.1e-117;
	Matches 579; Conservative	0; Mismatches 3; Indels 0; Gaps 0;
Qy	1	CTTTAAACAATTATTTTTATCTTCTTGTTGTCCTCTTCTCTCTTCTCTCATCACTATGA 60
Db	33	CTTTAAACAATTATTTTTATCTTCTTGTTGTCCTCTTCTCTTCTCTCATCACTATGA 92
Qy	61	AGAGTTTCAACACAGAAGGACACAAACACTCCACGGCGGAATCGGGGATGCCTCACCG 120
Db	93	AGAGTTTCAACACAGAAGGACACAAACACTCCACGGCGGAATCGGGGATGCCTCACCG 152
Qy	121	TGTGCGACC CGGACAAAGAACGTGCATGAAGATGTCGAGAGAGACGTACCGGACGTGCGC 180
Db	153	TGTGCGACC CGGACAAAGAACGTGCATGAAGATGTCGAGAGAGACGTACCGGACGTGCGC 212
Qy	181	TTACGGCGAGTCGGCATATATACACGGGGTGATAGGCTCGGAGTGTTGCTTTTAGCAT 240
Db	213	TTACGGCGAGTCGGCATATATACACGGGGTGATAGGCTCGGAGTGTTGCTTTTAGCAT 272
Qy	241	GGGCTATAGCTCAGCTTCGGTTGGATCGCAGGACATCGATCTTACTCATTTTCTCGTTCA 300
Db	273	GGGCTATAGCTCAGCTTCGGTTGGATCGCAGGACATCGATCTTACTCATTTTCTCGTTCA 332
Qy	301	TTACTTTACTTTCACCTCCACCATGCTTGCCGATGCTACCGTGCGCGGATCCGGTCACCG 360
Db	333	TTACTTTACTTTCACCTCCACCATGCTTGCCGATGCTACCGTGCGCGGATCCGGTCACCG 392
Qy	361	GAAAACGGAATTACACTTTACATGAGACGTTGTTTGATCTTACCTCGGTGGTAGAAGTGC 420
Db	393	GAAAACGGAATTACACTTTACATGAGACGTTGTTTGATCTTACCTCGGTGGTAGAAGTGC 452
Qy	421	AGCTCTGTGGAGTGGCACAAATATGGGAATCTGATTGGGGTCACTGTTGGTTACACCATCA 480
Db	453	AGCTCTGTGGAGTGGCACAAATATGGGAATCTGATTGGGGTCACTGTTGGTTACACCATCA 512
Qy	481	CTGCTCTTAATTAGTTTGGTAGGGTAGGGAATCGACATGCTTCCACGATAAAGGGCACA 540
Db	513	CTGCTCTTAATTAGTTTGGTAGGGTAGGGAATCGAATCTGCTTNACAGTAAGGGGCACA 572
Qy	541	CTGCCGAA TTGTA TACTATACGGAATTATCCGTATATGGCGGTTT 582
Db	573	CTGCCGAA TTGTA TACTATACGGAATTATCCGTATATGGNGGTTT 614

RESULT 2	AI995511/c	545 bp	linear	EST 08-SEP-1999
LOCUS	AI995511	701675547	A. thaliana, Columbia Col-0	inframe
DEFINITION	thaliana cDNA clone 701675547	701675547	701675547	Arabidopsis thaliana cDNA clone 701675547, mRNA sequence.
ACCESSION	AI995511			
VERSION	AI995511.1			
KEYWORDS	EST.	GI:5842496		

thale cress.

**SOURCE**  
ORGANISM Arabidopsis thaliana  
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eutrosids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 545)

**REFERENCE**  
AUTHORS Chen, J., Moniyama, M., Chan, E., Mooney, M., Carroon, B., Gilliland, D.,  
Wang, X., Hillman, J., Guegler, K., Kim, C., Doyle, M., Brzoska, P.,  
Gorgone, G., Burns, D., Griffin, J., Mouanoutoua, M., Nguyen, D., Tan, R.,  
Rose, M., Warren, B., Ton, B., Kastury, K., Borillo, C., Carpio, T.,  
Policky, J., Suzuki, G., Argentine, C., Shah, S., Nobruga, A., Murry, L.,  
Turner, C., Krikorian, S., Elder, L. and Hanson, D.  
TITLE Arabidopsis thaliana Gene Expression MicroArray  
Unpublished (1999)  
CONTACT: David Smoller, Ph.D.  
Genome Systems, Inc., a wholly owned subsidiary of Incyte  
Pharmaceuticals, Inc.  
4633 World Parkway Circle, St. Louis, MO 63134, USA  
Tel: 877-577-2733  
Fax: 314-427-3324  
Email: service@genomesystems.com.

**FEATURES**  
source  
1..545  
/organism="Arabidopsis thaliana"  
/cultivar="Columbia Col-0"  
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/clone="701675547"  
/clone\_lib="A. thaliana, Columbia Col-0, inflorescence-1"  
/tissue\_type="inflorescence"  
/dev\_stage="4 - 7 weeks"  
/note="Vector: pSPORT; Site 1: NotI; Site 2: SalI; cDNA  
library was derived from untreated inflorescence tissue  
from Arabidopsis thaliana, Columbia Col-0, at 4 - 7  
weeks. Plants were grown in 1:1:1 peat  
moas/vermiculite/perlite soil at 22 deg. C +/- 3 deg. C  
under constant light, and watered with fertilizer. cDNA  
synthesis was initiated using a NotI-oligo(dT) primer.  
Double-stranded cDNA was blunted, ligated to SalI adaptore,  
digested with NotI, size-selected, and cloned into the  
NotI and SalI sites of the pSPORT vector."

BASE COUNT	169 a	105 c	110 g	149 t	12 others
ORIGIN					
Query Match	28.1%	Score 473.8;	DB 9;	Length 545;	
Best Local Similarity	95.9%	Pred. NO. 3.6e-94;			
Matches 512; Conservative	0;	Mismatches 18;	Indels 4;	Gaps 3;	
QY	1119	AAAAAATGCAACAGAAACTATCC--AGACACACAAAGTTCATCACTCTCTGAAATATTCAGTAA	1176		
Db	534	AAAAATGCAACAGAAACTATCCAGACACACCAAGTNCATCACTCTCTGAAATATTCAGTAA	475		
QY	1177	AGGTACCTTTCTTGGAATAATCAACATTAAGCTCTTCAGATTGGTGGAGAGACAGTTT	1236		
Db	474	AGGTACCTTTCTTGGAATAATCAACATTAAGCTCTTCAGATTGGTGGAGAGACAGTTT	415		
QY	1237	ATGTGGTTATAACCACTGTTGTAGCTATGATATTCCTTTCTTCAACCGCATCTTAGGTCT	1296		
Db	414	ATGTGGTTATAACCACTGTTGTAGCTATGATATTCCTTTCTTCAACCGCATCTTAGGTCT	355		
QY	1297	TTTATCGAGACAGCTTCCTTTCTGGGCTTTAACGGTTTATTTCCCTGTGGAGATGCACATTG	1356		
Db	354	TTTATCGAGACAGCTTCCTTTCTGGGCTTTAACGGTTTATATCCCTGTGGAGATGCACATTG	295		
QY	1357	GACAAACCAAGATTAAAGAGTACTCTGCTAGATGGAATGGCTGAAACGATGTGCTATG	1416		
Db	294	GACAAACCAAGATTAAAGAGTACTCTGCTAGATGGAATGGCTGAAACGATGTGCTATG	235		
QY	1417	TTTGTGTTGATCGTCTGCGTCTTTAGTTCGACCCGGATCCATTCGACGACTTATAAGTAGTG	1476		
Db	234	TTTGTGTTGATCGTCTGCGTCTTTAGTTCGACCCGGATCCATTCGACGACTTATAAGTAGTG	175		
QY	1477	TCAAAACCTTACAAGCCCTTCCGAGACTATGCA-TGAGTGAAGTT--TGAGATCTCTCAAGAGAG	1534		

Db 174 TCAAAACCTACAGCCCTCCGACATATGACANNAGTGGATGAGATCCCTCAAGAG 115  
 Oy 1535 TCAAAAATATATAGTAGTTGGTCTTCTCTTTAAACATATGCTGTCTAAATCCAAATG 1594  
 Db 114 TCAAAAATATATAGTAGTTGGTCTTCTCTTTAAACATATGCTGTCTAAATCCAAATG 55  
 Oy 1595 AGAATGCTTATATGCTTAAACCTCATGAATCTCTCTGTATCTTAACTTTCAAT 1648  
 Db 54 AGAATGCTTATATGCTTAAACCTCATGAATCTCTCTGTATCTTAACTTTCAAT 1

RESULT 3  
 AV796991/c 434 bp mRNA linear EST 29-MAR-2002  
 LOCUS AV796991 RAFL9 Arabidopsis thaliana cDNA clone RAFL9-10-P18 3',  
 DEFINITION mRNA sequence.  
 AV796991  
 VERSION AV796991.1 GI:19830974  
 KEYWORDS EST.  
 SOURCE chae cress.  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 1 (bases 1 to 434)  
 REFERENCE Oono, Y., Sakurai, T., Carninci, P., Kamiya, A., Satou, M., Nakajima, M.,  
 Akiyama, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.  
 and Shinozaki, K.  
 Large scale analysis of Arabidopsis full-length cDNA (2002b)  
 TITLE Unpublished (2002)  
 JOURNAL Contact: Motoaki Seki  
 COMMENT Plant Functional Genomics Research Group  
 RIKEN Genomic Sciences Center  
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
 Tel: 81-298-36-4359  
 Fax: 81-298-36-9060  
 Email: mseki@rcc.riken.go.jp  
 An Arabidopsis full-length cDNA library was constructed essentially  
 as reported previously (Seki et al., 1998). cDNA cleaved with BamHI  
 and XhoI was ligated to modified lambda FLIC-1 vector (Carninci et  
 al., submitted for publication) digested with BamHI and SalI. This  
 clone is in a modified Bluescript vector. Please visit our web  
 site (http://www.gsc.riken.go.jp/e/plant/index\_e.html) for further  
 details.

FEATURES  
 source  
 Location/Qualifiers  
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 /organism="Arabidopsis thaliana"  
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 dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24  
 hr) treatments"  
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 ORIGIN

Query Match 25.8%; Score 434; DB 10; Length 434;  
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 Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1177 ACAGACCTTCTGGAATATGACATTTAGCTCTTCAGATTTGGTGGAGAGAGAGCTT 1236  
 Db 434 ACAGACCTTCTGGAATATGACATTTAGCTCTTCAGATTTGGTGGAGAGAGAGCTT 375  
 Oy 1237 ATGGGTATTAACCACTGTGTGATGATATATTCCTTTCTTCAACGAGATCTTAGGTC 1296  
 Db 374 ATGGGTATTAACCACTGTGTGATGATATATTCCTTTCTTCAACGAGATCTTAGGTC 315  
 Oy 1297 TTATGGAGCAGCTTCTTGGCCCTTAACGGTTATATTCCTGTGGAGATGACATTTG 1356

Db 314 TTATCGAGCAGGCTTCCCTTCTGACCTTTAAGCTTTATTTCCCTGTGAGATGACAAATTTG 255  
 Oy 1357 CACAACCAAGATTAAAGATCTCTGTAGATGATGATGATGATGATGATGATGATGATG 1416  
 Db 254 CACAACCAAGATTAAAGATCTCTGTAGATGATGATGATGATGATGATGATGATGATG 195  
 Oy 1417 TTTCCTGATGCTGTGCTCTTTAGCTGACCGGATTCATGCGACAGACTTAAATAGTGTG 1476  
 Db 194 TTTCCTGATGCTGTGCTCTTTAGCTGACCGGATTCATGCGACAGACTTAAATAGTGTG 135

Oy 1477 TCAAAACCTACAGCCCTCCGACATATGATGATGATGATGATGATGATGATGATGATG 1536  
 Db 134 TCAAAACCTACAGCCCTCCGACATATGATGATGATGATGATGATGATGATGATGATG 75  
 Oy 1537 AAAATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1596  
 Db 74 AAAATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 15

Oy 1597 AATGCTTATTTGCT 1610  
 Db 14 AATGCTTATTTGCT 1

RESULT 4  
 AV804261/c 418 bp mRNA linear EST 29-MAR-2002  
 LOCUS AV804261 RAFL9 Arabidopsis thaliana cDNA clone RAFL9-38-H12 3',  
 DEFINITION mRNA sequence.  
 AV804261  
 VERSION AV804261.1 GI:19838246  
 KEYWORDS EST.  
 SOURCE chae cress.  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 1 (bases 1 to 418)  
 REFERENCE Oono, Y., Sakurai, T., Carninci, P., Kamiya, A., Satou, M., Nakajima, M.,  
 Akiyama, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.  
 and Shinozaki, K.  
 Large scale analysis of Arabidopsis full-length cDNA (2002b)  
 TITLE Unpublished (2002)  
 JOURNAL Contact: Motoaki Seki  
 COMMENT Plant Functional Genomics Research Group  
 RIKEN Genomic Sciences Center  
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
 Tel: 81-298-36-4359  
 Fax: 81-298-36-9060  
 Email: mseki@rcc.riken.go.jp  
 An Arabidopsis full-length cDNA library was constructed essentially  
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 al., submitted for publication) digested with BamHI and SalI. This  
 clone is in a modified Bluescript vector. Please visit our web  
 site (http://www.gsc.riken.go.jp/e/plant/index\_e.html) for further  
 details.

FEATURES  
 source  
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 /organism="Arabidopsis thaliana"  
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 /lab\_host="DH10B"  
 /note="Site 1: BamHI; Site 2: SalI; subjected to  
 dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24  
 hr) treatments"  
 BASE COUNT 140 a 81 c 89 g 108 t  
 ORIGIN

Query Match 24.7%; Score 416.4; DB 10; Length 418;  
Best Local Similarity 99.8%; Pred. No. 1.7e-81;  
Matches 417; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1252 CTGTTGTAGCTATCATATCCCTTTCTTCAACCGCATCTTAGTCTTATCGGAGCAGCTT 1311  
DB 418 CTGTTGTAGCTATCATATCCCTTTCTTCAACCGCATCTTAGTCTTATCGGAGCAGCTT 359

QY 1312 CTTCTGCGCTTTAAACGGTTATTTCCCTGTGGAGATGACATTCGACAAACCAAGATTA 1371  
DB 358 CTTCTGCGCTTTAAACGGTTATTTCCCTGTGGAGATGACATTCGACAAACCAAGATTA 299

QY 1372 AGAAGTACTCTGCTAGATGATTCGCTGAAACCGATGCTATGTTTGTGTTGATCGTCT 1431  
DB 298 AGAAGTACTCTGCTAGATGATTCGCTGAAACCGATGCTATGTTTGTGTTGATCGTCT 239

QY 1432 CGCTCTTAGCTGACGCGGATCCATGCGAGGACTTAAAGTAGTGTCAAAACCTACAAAGC 1491  
DB 238 CGCTCTTAGCTGACGCGGATCCATGCGAGGACTTAAAGTAGTGTCAAAACCTACAAAGC 179

QY 1492 CTTCCGAGCTATCATGAGTGTGAGTTCCTCAAGAGAGTCAAAAATATATGTAGT 1551  
DB 178 CTTCCGAGCTATCATGAGTGTGAGTTCCTCAAGAGAGTCAAAAATATATGTAGT 119

QY 1552 AGTTTGTCTTTCTGTTAAACTATCTGTGCTTAAATCCATGAGATGCTTTTATGCTA 1611  
DB 118 AGTTTGTCTTTCTGTTAAACTATCTGTGCTTAAATCCATGAGATGCTTTTATGCTA 59

QY 1612 AAACCTTCATGAATCTCTCTGATCTACATCTTTCAATCTTAATACATATGAGTCTTCC 1669  
DB 58 AAACCTTCATGAATCTCTCTGATCTACATCTTTCAATCTTAATACATATGAGTCTTCTC 1

RESULT 5  
AV803440/c  
LOCUS AV803440 RAFL9 Arabidopsis thaliana cDNA clone RAFL09-35-112 3',  
DEFINITION mRNA sequence.  
ACCESSION AV803440  
VERSION AV803440.1 GI:19837425  
KEYWORDS EST.  
SOURCE thale cress.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
REFERENCE 1 (bases 1 to 415)  
Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,  
Ono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,  
Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.  
and Shinozaki, K.  
Large scale analysis of Arabidopsis full-length cDNA (2002b)  
Unpublished (2002)  
Contact: Motoaki Seki  
Plant Functional Genomics Research Group  
RIKEN Genomic Sciences Center  
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
Tel: 81-298-36-4359  
Fax: 81-298-36-9060  
Email: mseki@rc.riken.go.jp  
An Arabidopsis full-length cDNA library was constructed essentially  
as reported previously (Seki et al., 1998). cDNA cleaved with BamHI  
and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et  
al., submitted for publication) digested with BamHI and SalI. This  
clone is in a modified phagescript vector. Please visit our web  
site ([http://www.gsc.riken.go.jp/e/plant/index\\_e.html](http://www.gsc.riken.go.jp/e/plant/index_e.html)) for further  
details.

FEATURES  
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/clone\_lib="RAFL9"

/dev\_stages="plants at various developmental stages from  
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/lab\_host="DH10B"  
/note="Site 1: BamHI; Site 2: SalI; subjected to  
dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24  
hr) treatments"

BASE COUNT 134 a 90 c 85 g 106 t  
ORIGIN

Query Match 24.6%; Score 415; DB 10; Length 415;  
Best Local Similarity 100.0%; Pred. No. 3.5e-81;  
Matches 415; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1195 AATTCAACATTAGCTCTTTCAGATTGGTGGAGGACAGCTTATGTGTTATACCACTG 1254  
DB 415 AATTCAACATTAGCTCTTTCAGATTGGTGGAGGACAGCTTATGTGTTATACCACTG 356

QY 1255 TTGTAGCTATGATTAATTCCTTTTCAACCGGATCTTAGTCTTATCGGAGAGCTTCCT 1314  
DB 355 TTGTAGCTATGATTAATTCCTTTTCAACCGGATCTTAGTCTTATCGGAGAGCTTCCT 296

QY 1315 TCTGCGCTTTAAACGGTTATTTCCCTGTGGAGATGCATTCGACAAACCAAGATTAGA 1374  
DB 295 TCTGCGCTTTAAACGGTTATTTCCCTGTGGAGATGCATTCGACAAACCAAGATTAGA 236

QY 1375 AGTACTCTGTAGATGATTCGCTGAAACCGATGCTATGTTTGTCTGATCGTTCGC 1434  
DB 235 AGTACTCTGTAGATGATTCGCTGAAACCGATGCTATGTTTGTCTGATCGTTCGC 176

QY 1435 TCTTAGCTGCGAGCGGATCCATGCGAGGACTTATAAGTAGTGTCAAAACCTACAAAGCCT 1494  
DB 175 TCTTAGCTGCGAGCGGATCCATGCGAGGACTTATAAGTAGTGTCAAAACCTACAAAGCCT 116

QY 1495 TCCGAGCTATGCATGAGTTCAGTTCGATTCCTCAAGAGAGTCAAAAATATATGATGAGT 1554  
DB 115 TCCGAGCTATGCATGAGTTCAGTTCGATTCCTCAAGAGAGTCAAAAATATATGATGAGT 56

QY 1555 TTGTCTCTTCTGTTAACTATCTGTTCTTAATCCATGAGATGCTTTTATTGTC 1609  
DB 55 TTGTCTCTTCTGTTAACTATCTGTTCTTAATCCATGAGATGCTTTTATTGTC 1

RESULT 6  
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LOCUS AV803032 RAFL9 Arabidopsis thaliana cDNA clone RAFL09-34-B17 3',  
DEFINITION mRNA sequence.  
ACCESSION AV803032  
VERSION AV803032.1 GI:19837017  
KEYWORDS EST.  
SOURCE thale cress.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
REFERENCE 1 (bases 1 to 414)  
Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,  
Ono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,  
Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.  
and Shinozaki, K.  
Large scale analysis of Arabidopsis full-length cDNA (2002b)  
Unpublished (2002)  
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RIKEN Genomic Sciences Center  
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
Tel: 81-298-36-4359  
Fax: 81-298-36-9060  
Email: mseki@rc.riken.go.jp  
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as reported previously (Seki et al., 1998). cDNA cleaved with BamHI  
and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et  
al., submitted for publication) digested with BamHI and SalI. This  
clone is in a modified phagescript vector. Please visit our web  
site ([http://www.gsc.riken.go.jp/e/plant/index\\_e.html](http://www.gsc.riken.go.jp/e/plant/index_e.html)) for further  
details.

FEATURES  
source  
1..415  
/organism="Arabidopsis thaliana"  
/db\_xref="taxon:3702"  
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/clone\_lib="RAFL9"



REFERENCE 1 (bases 1 to 407)  
 AUTHORS Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,  
 Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y.,  
 Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y.  
 and Shinozaki,K.  
 TITLE Large scale analysis of Arabidopsis full-length cDNA (2002b)  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Motoaki Seki  
 Plant Functional Genomics Research Group  
 RIKEN Genomic Sciences Center  
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 Fax: 81-298-36-9060  
 Email: msek@rc.riken.go.jp  
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 details.

FEATURES Location/Qualifiers  
 source 1..407  
 /organism="Arabidopsis thaliana"  
 /db\_xref="taxon:3702"  
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 /clone\_lib="RAFL9"  
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 germination to mature seeds"  
 /lab\_host="DH10B"  
 /note="Site 1: BamHI; Site 2: SalI; subjected to  
 dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24  
 hr) treatments"  
 BASE COUNT 134 a 78 c 88 g 107 t  
 ORIGIN

Query Match 24.2%; Score 407; DB 10; Length 407;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-79;  
 Matches 407; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1263 ATGATATCCCTTTCTTCAACCGGATCTTAGTCTTATCGGAGCAGCTTCCTTCGGCCT 1322  
 Db 407 ATGATATCCCTTTCTTCAACCGGATCTTAGTCTTATCGGAGCAGCTTCCTTCGGCCT 348  
 Qy 1323 TTAACGGTTTATTTCCCTGTGGAGATGCATTCGACAAACCAAGATTAAAGTACTCT 1382  
 Db 347 TTAACGGTTTATTTCCCTGTGGAGATGCATTCGACAAACCAAGATTAAAGTACTCT 288  
 Qy 1383 GCTAGATGGATTCGCTGAAACCGATGCTATGTTTGGTTCGCTCTCTAGCT 1442  
 Db 287 GCTAGATGGATTCGCTGAAACCGATGCTATGTTTGGTTCGCTCTCTAGCT 228  
 Qy 1443 GCAGCCGATCCATCGCAGACTTATAAGTAGTGTCAAAACCTCAAGCCCTTCGGACT 1502  
 Db 227 GCAGCCGATCCATCGCAGACTTATAAGTAGTGTCAAAACCTCAAGCCCTTCGGACT 168  
 Qy 1503 ATGCATGAGTGAGTTTGAGATCTCTCAAGAGAGTCAAAATATATGATGTTGGTCTT 1562  
 Db 167 ATGCATGAGTGAGTTTGAGATCTCTCAAGAGAGTCAAAATATATGATGTTGGTCTT 108  
 Qy 1563 TCTGTAAACCTATCTGCTGTCTAAATCCATGAGATGCTTTATTGCTTAAACCTTCATGA 1622  
 Db 107 TCTGTAAACCTATCTGCTGTCTAAATCCATGAGATGCTTTATTGCTTAAACCTTCATGA 48  
 Qy 1623 ATCTCTGTGATCTACATCTTTCAATCTAATACATGAGCTCTTCC 1669  
 Db 47 ATCTCTGTGATCTACATCTTTCAATCTAATACATGAGCTCTTCC 1

RESULT 9  
 AV810513/c 421 bp mRNA linear EST 29-MAR-2002  
 LOCUS AV810513  
 DEFINITION AV810513 RAFL9 Arabidopsis thaliana cDNA clone RAFL09-84-D24 3',

ACCSSION AV810513  
 VERSION AV810513.1 GI:19844498  
 KEYWORDS EST.  
 SOURCE ORGANISM  
 Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; euroids II; Brassicales; Brassicaceae; Arabidopsi.  
 1 (bases 1 to 421)  
 REFERENCE  
 AUTHORS Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,  
 Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y.,  
 Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y.  
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 details.

FEATURES Location/Qualifiers  
 source 1..421  
 /organism="Arabidopsis thaliana"  
 /db\_xref="taxon:3702"  
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 /clone\_lib="RAFL9"  
 /dev\_stage="plants at various developmental stages from  
 germination to mature seeds"  
 /note="Site 1: BamHI; Site 2: SalI; subjected to  
 dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24  
 hr) treatments"  
 BASE COUNT 143 a 78 c 91 g 109 t  
 ORIGIN

Query Match 24.0%; Score 404.8; DB 10; Length 421;  
 Best Local Similarity 98.3%; Pred. No. 6.2e-79;  
 Matches 409; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
 Qy 1256 TGTAGCTATGATATCCCTTTCTTCAACCGGATCTTAGTCTTATCGGAGCAGCTTCCTT 1315  
 Db 418 TTAGCTATGATATCCCTTTCTTCAACCGGATCTTAGTCTTATCGGAGCAGCTTCCTT 359  
 Qy 1316 CTGSCCTTTAAAGTTTATTTCCCTGTGAGATGCACATTCACAAAACCAAGATTAGAA 1375  
 Db 358 CTGSCCTTTAAAGTTTATTTCCCTGTGAGATGCACATTCACAAAACCAAGATTAGAA 299  
 Qy 1376 GTACTCTGTAGATGAGTTCGCTGAAAACGATGCTGCTATGTTTGTGTCGCTCGCT 1435  
 Db 298 GTACTCTGTAGATGAGTTCGCTGAAAACGATGCTGCTATGTTTGTGTCGCTCGCT 239  
 Qy 1436 CTTAGCTGACGCGGATCCATCGAGGACTTATAGTAGTGTCAAAAACCTACAGCCCTT 1495  
 Db 238 CTTAGCTGACGCGGATCCATCGAGGACTTATAGTAGTGTCAAAAACCTACAGCCCTT 179  
 Qy 1496 CCGACTATGCATGAGTGTGAGTTGAGATCTTCAGAGAGTCAAAAATATATGTAGTAGTT 1555  
 Db 178 CCGACTATGCATGAGTGTGAGTTGAGATCTTCAGAGAGTCAAAAATATATGTAGTAGTT 119  
 Qy 1556 TGGTCTTCTGTTAAACTATCTGGTCTCTAAATCAAGTGAATGCTTTATTGCTAAAC 1615  
 Db 118 TGGTCTTCTGTTAAACTATCTGGTCTCTAAATCAAGTGAATGCTTTATTGCTAAAC 59



QY 1616 TTCAATGATCTCTCTGATCATCTTCAATCTAATACATAGAGCTTTCCAA 1671  
 DB 58 TTCAATGATCTCTCTGATCATCTTCAATCTAATACATAGAGCTTTCCAA 3  
  
 RESULT 10  
 AV818296/c 419 bp mRNA linear EST 01-APR-2002  
 LOCUS AV818296 RAFL9 Arabidopsis thaliana cDNA clone RAFL09-97-j12 3',  
 DEFINITION mRNA sequence.  
 ACCESSION AV818296  
 VERSION AV818296.1 GI:19860206  
 KEYWORDS EST,  
 SOURCE thale cress.  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 1 (bases 1 to 419)  
 REFERENCE Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,  
 Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,  
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 al., submitted for publication) digested with BamHI and SalI. This  
 clone is in a modified Bluescript vector. Please visit our web  
 site (http://www.gsc.riken.go.jp/e/plant/index\_e.html) for further  
 details.  
 FEATURES  
 source location/Qualifiers  
 1..419  
 /organism="Arabidopsis thaliana"  
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 /clone="RAFL09-97-012"  
 /clone\_lib="RAFL9"  
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 germination to mature seeds"  
 /lab\_host="DH10B"  
 /note="Site 1: BamHI; Site 2: SalI; subjected to  
 dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24  
 hr) treatments"  
 BASE COUNT 136 a 89 c 88 g 106 t  
 ORIGIN  
 Query Match 23.9%; Score 402; DB 10; Length 419;  
 Best Local Similarity 99.8%; Pred. No. 2.6e-78;  
 Matches 413; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 QY 1166 ATATTCAGTAACGTAACCTTCTTGGAATTCACATTAAGCTTTCAGATGGTGTG 1225  
 DB 414 ATATTCAGTAACGTAACCTTCTTGGAATTCACATTAAGCTTTCAGATGGTGTG 356  
 QY 1226 GAGGACAGCTATGTGTTTAACCACTGTTAGCTATGATATTCCTTTTCAAGCG 1285  
 DB 355 GAGGACAGCTATGTGTTTAACCACTGTTAGCTATGATATTCCTTTTCAAGCG 296  
 QY 1286 GATCTTAGGTCCTTACGAGAGCTTCTTGGCCCTTAACGGTTATTTCCCTGTGGA 1345  
 DB 295 GATCTTAGGTCCTTACGAGAGCTTCTTGGCCCTTAACGGTTATTTCCCTGTGGA 236  
 QY 1346 GATGACATTCGACAAACCAAGATTAGAAGTCTGCTAGATGGATTGCGCTGAAC 1405  
 DB 235 GATGACATTCGACAAACCAAGATTAGAAGTCTGCTAGATGGATTGCGCTGAAC 176

QY 1406 GATGTCATGTTTGGCTGTAATGCTGCTTACCTGACCGGATCCATCGAGAGACT 1465  
 DB 175 GATGTCATGTTTGGCTGTAATGCTGCTTACCTGACCGGATCCATCGAGAGACT 116  
 QY 1466 TATAAGTAGTGTCAAAACCTACAGCCCTTCCGACCTATGACATGATGATTGATCC 1525  
 DB 115 TATAAGTAGTGTCAAAACCTACAGCCCTTCCGACCTATGACATGATGATTGATCC 56  
 QY 1526 TCAAGAGATGCAAAAATATATGTAGTAGTTGGTCTTCTGTTAATCATATCTGG 1579  
 DB 55 TCAAGAGATGCAAAAATATATGTAGTAGTTGGTCTTCTGTTAATCATATCTGG 2  
  
 RESULT 11  
 AV814816/c 408 bp mRNA linear EST 01-APR-2002  
 LOCUS AV814816 RAFL9 Arabidopsis thaliana cDNA clone RAFL09-84-F17 3',  
 DEFINITION mRNA sequence.  
 ACCESSION AV814816  
 VERSION AV814816.1 GI:19856625  
 KEYWORDS EST,  
 SOURCE thale cress.  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 1 (bases 1 to 408)  
 REFERENCE Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,  
 Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,  
 Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.,  
 and Shinozaki, K.  
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 TITLE Unpublished (2002)  
 JOURNAL Contact: Motoaki Seki  
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 clone is in a modified Bluescript vector. Please visit our web  
 site (http://www.gsc.riken.go.jp/e/plant/index\_e.html) for further  
 details.  
 FEATURES  
 source location/Qualifiers  
 1..408  
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 /clone\_lib="RAFL9"  
 /dev\_stage="plants at various developmental stages from  
 germination to mature seeds"  
 /lab\_host="DH10B"  
 /note="Site 1: BamHI; Site 2: SalI; subjected to  
 dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24  
 hr) treatments"  
 BASE COUNT 134 a 79 c 88 g 107 t  
 ORIGIN  
 Query Match 23.5%; Score 396; DB 10; Length 408;  
 Best Local Similarity 99.8%; Pred. No. 5.4e-77;  
 Matches 407; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 QY 1263 ATGATATTCCTTTCTTCAACGAGATCTTAGGCTTATGAGACAGCTTCTTGAGCT 1322  
 DB 408 ATGATATTCCTTTCTTCAACGAGATCTTAGGCTTATGAGACAGCTTCTTGAGCT 349  
 QY 1323 TTAACGTTTATTTCCCTGAGAGATGACATTCGACAAACCAAGATTAGAAGTACT 1382

Db 348 TTAACGGTTATTTCCCTGTGGAGATGCACATTGCCAAACCAAGATTAAAGACTACTCT 289  
 QY 1383 GCTAGATGATTTGGCGTGAACAGATGTGCTATGTTTGTGCTGCTCGCTCTTAGCT 1442  
 Db 288 GCTAGATGATTTGGCGTGAACAGATGTGCTATGTTTGTGCTGCTCGCTCTTAGCT 229  
 QY 1443 GCA-GCCGGATCCATCCAGGACTTAAGTAGTGTCAAAACCTACRAGCCCTCCCGAC 1501  
 Db 228 GCAGCCGGATCCATCCAGGACTTAAGTAGTGTCAAAACCTACRAGCCCTCCCGAC 169  
 QY 1502 TATGATGAGTGAGTTTGGATCCTCAAGAGAGTCAAAATATATATAGTAGTTGGTCT 1561  
 Db 168 TATGATGAGTGAGTTTGGATCCTCAAGAGAGTCAAAATATATATAGTAGTTGGTCT 109  
 QY 1562 TTCTGTTAAACTATCTCGTCTCAATCCAAATGAGAAATGCTTTATGCTTAAACTTCATG 1621  
 Db 108 TTCTGTTAAACTATCTCGTCTCAATCCAAATGAGAAATGCTTTATGCTTAAACTTCATG 49  
 QY 1622 AATCTCTGTATACATCTTTCAATCTAATACATATGAGCTCTTCC 1669  
 Db 48 AATCTCTGTATACATCTTTCAATCTAATACATATGAGCTCTTCC 1

RESULT 12  
 AV812283/c  
 LOCUS AV812283 RAFL9 Arabidopsis thaliana cDNA clone RAFL09-72-K15 3',  
 DEFINITION mRNA sequence.  
 ACCESSION AV812283  
 VERSION AV812283.1 GI:19846268  
 KEYWORDS EST.  
 SOURCE thale cress.

ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 REFERENCE 1 (bases 1 to 405)  
 AUTHORS Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,  
 Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,  
 Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.  
 and Shinozaki, K.

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 JOURNAL Unpublished (2002)  
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Email: mseki@rtc.riken.go.jp  
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 details.

FEATURES Location/Qualifiers  
 source 1..405  
 /organism="Arabidopsis thaliana"  
 /db\_xref="taxon:3702"  
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 /clone\_lib="RAFL9"  
 /dev\_stage="plants at various developmental stages from  
 germination to mature seeds"  
 /lab\_host="DH108"  
 /note="Site 1: BamHI; Site 2: SalI; subjected to  
 dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24  
 hr) treatments"  
 BASE COUNT 131 a 78 c 85 g 111 t

Query Match 23.4%; Score 394.8; DB 10; Length 405;

Best Local Similarity 99.5%; Pred. No. le-76;  
 Matches 396; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1280 CAACGCGATCTTAGTCTTTATCGGAGCAGCTTCTCTTGGCCTTTAAACGGTTTATTTCCC 1339  
 Db 405 CAACGCGATCTTAGTCTTTATCGGAGCAGCTTCTCTTGGCCTTTAAACGGTTTATTTCCC 346  
 QY 1340 TGTGGAGATGCACATTGGCAAAACCAAGATTAAAGAGTACTCTGCTAGATGAGATGGCT 1399  
 Db 345 TGTGGAGATGCACATTGGCAAAACCAAGATTAAAGAGTACTCTGCTAGATGAGATGGCT 286  
 QY 1400 GAAACCATGTGCTATGTTTGTGCTGCTCTCTTCTAGCTGCAGCCGATCCATCGC 1459  
 Db 285 GAAACCATGTGCTATGTTTGTGCTGCTCTCTTCTAGCTGCAGCCGATCCATCGC 226  
 QY 1460 AGGCTTTAAGTAGTGTCAAAACCTACAGCCCTTCGGACTATGATGATGAGTTTG 1519  
 Db 225 AGGCTTTAAGTAGTGTCAAAACCTACAGCCCTTCGGACTATGATGATGAGTTTG 166  
 QY 1520 AGATCTCTCAAGAGAGTCAAAATATATGATAGTAGTTGGTCTTCTGTTAAACTATCTGG 1579  
 Db 165 AGATCTCTCAAGAGAGTCAAAATATATGATAGTAGTTGGTCTTCTGTTAAACTATCTGG 106  
 QY 1580 TGTCTAAATCCATGAGATGCTTTTATGCTTAAACTCATGATCTCTCTGTATCTACA 1639  
 Db 105 TGTCTAAATCCATGAGATGCTTTTATGCTTAAACTCATGATCTCTCTGTATCTACA 46  
 QY 1640 TCTTTCAATCTAATACATATGATGAGCTCTTCCAAAAAAA 1677  
 Db 45 TCTTTCAATCTAATACATATGATGAGCTCTTCCAAATATA 8

RESULT 13  
 AV802054/c  
 LOCUS AV802054 RAFL9 Arabidopsis thaliana cDNA clone RAFL09-30-I10 3',  
 DEFINITION mRNA sequence.  
 ACCESSION AV802054  
 VERSION AV802054.1 GI:19836039  
 KEYWORDS EST.  
 SOURCE thale cress.

ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

REFERENCE 1 (bases 1 to 391)  
 AUTHORS Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,  
 Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,  
 Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.  
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Email: mseki@rtc.riken.go.jp  
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 details.

FEATURES Location/Qualifiers  
 source 1..391  
 /organism="Arabidopsis thaliana"  
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 /clone="RAFL09-30-I10"  
 /clone\_lib="RAFL9"  
 /dev\_stage="plants at various developmental stages from

germination to mature seeds"

/lab host="DH10B"  
/note="Site 1: BamHI; Site 2: SalI; subjected to  
dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24  
hr) treatments"

BASE COUNT 125 a 84 c 80 g 102 t  
ORIGIN

Query Match 23.2%; Score 391; DB 10; Length 391;  
Best Local Similarity 100.0%; Pred. No. 7e-76;  
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1226 GAGACAGCTTATGTTGTTTAAACACTGTTGATGATATATCCCTTCTTCAACGC 1285  
Db 391 GAGACAGCTTATGTTGTTTAAACACTGTTGATGATATATCCCTTCTTCAACGC 332  
Oy 1286 GATCTTAGGTTCTTACGAGAGCTTCTTGGCTTAAAGCTTTATTTCCCGTGGGA 1345  
Db 331 GATCTTAGGTTCTTACGAGAGCTTCTTGGCTTAAAGCTTTATTTCCCGTGGGA 272  
Oy 1346 GATGCACTTTCACAAACCAAGTAAAGTAACTCTGCTAATGATGATGCTGAAAC 1405  
Db 271 GATGCACTTTCACAAACCAAGTAAAGTAACTCTGCTAATGATGATGCTGAAAC 212  
Oy 1406 GATGCTATGTTGCTTGAATCGTCTGCTTACGCTGAGCGGATCATGCGAGACT 1465  
Db 211 GATGCTATGTTGCTTGAATCGTCTGCTTACGCTGAGCGGATCATGCGAGACT 152  
Oy 1466 TATAAGTAGTCAAAACCTTCAAGCCCTTCCGACTATGATGATGATGATGATGAT 1525  
Db 151 TATAAGTAGTCAAAACCTTCAAGCCCTTCCGACTATGATGATGATGATGATGAT 92  
Oy 1526 TCAAGAGAGTCAAAATATATATAGTATGTTGTTGTTGTTGTTGTTGTTGTTGTTA 1585  
Db 91 TCAAGAGAGTCAAAATATATATAGTATGTTGTTGTTGTTGTTGTTGTTGTTGTTA 32  
Oy 1586 AATCCATGAGATGCTTTATTTGCTAAACT 1616  
Db 31 AATCCATGAGATGCTTTATTTGCTAAACT 1

RESULT 14  
AV800991/c 401 bp mRNA linear EST 29-MAR-2002  
LOCUS AV800991  
DEFINITION AV800991 RAFL9 Arabidopsis thaliana cDNA clone RAFL09-26-F16 3',  
mRNA sequence.  
ACCESSION AV800991  
VERSION AV800991.1 GI:19834976  
KEYWORDS EST.  
SOURCE thale cress.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eustosids II; Brassicales; Brassicaceae; Arabidopsids.  
1 (bases 1 to 401)  
Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,  
Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,  
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Fax: 81-298-36-9060

TITLE  
JOURNAL  
COMMENT  
Email: meki@rcc.riken.go.jp  
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details.

FEATURES Location/Qualifiers  
source 1..401  
/organism="Arabidopsis thaliana"  
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ORIGIN

Query Match 23.1%; Score 389; DB 10; Length 401;  
Best Local Similarity 99.8%; Pred. No. 1.9e-75;  
Matches 400; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Oy 1270 TCCCTTCTTCAAGCGATCTTATGCTTATGAGACAGCTTCTTGGCTTTAAACG 1329  
Db 401 TCCCTTCTTCAAGCGATCTTATGCTTATGAGACAGCTTCTTGGCTTTAAACG 342  
Oy 1330 TTTATTTCCCTGAGAGATGACATGACAAACCAAGTTAAGAACTCTGCTGAT 1389  
Db 341 TTTATTTCCCTGAGAGATGACATGACAAACCAAGTTAAGAACTCTGCTGAT 282  
Oy 1390 GGAATGCGCTGAAACGAGTGTCTATGTTGCTTGAATGCTCTGCTTATGCTGAGCG 1449  
Db 281 GGAATGCGCTGAAACGAGTGTCTATGTTGCTTGAATGCTCTGCTTATGCTGAGCG 222  
Oy 1450 GATCCATGCGAGACTTATAGTA-GTGTCAAAACCTCAAGCCCTTCCGACTATGAT 1508  
Db 221 GATCCATGCGAGACTTATAGTA-GTGTCAAAACCTCAAGCCCTTCCGACTATGAT 162  
Oy 1509 GAGTGAGTTGAGATCTCTCAAGAGTCAAAATATATAGTATGATGTTGCTTCTGTT 1568  
Db 161 GAGTGAGTTGAGATCTCTCAAGAGTCAAAATATATAGTATGATGTTGCTTCTGTT 102  
Oy 1569 AAACATCTGCTCTTAAATCCCAATGAGATGTTATGCTTAAACCTCAAGATCTCT 1628  
Db 101 AAACATCTGCTCTTAAATCCCAATGAGATGTTATGCTTAAACCTCAAGATCTCT 42  
Oy 1629 CTGTATCTACATCTTCAATCTATATGATGAGCTCTTCC 1669  
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RESULT 15  
AV820975/c 405 bp mRNA linear EST 01-APR-2002  
LOCUS AV820975  
DEFINITION AV820975 RAFL11 Arabidopsis thaliana cDNA clone RAFL11-13-F24 3',  
mRNA sequence.  
ACCESSION AV820975  
VERSION AV820975.1 GI:19862988  
KEYWORDS EST.  
SOURCE thale cress.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eustosids II; Brassicales; Brassicaceae; Arabidopsids.  
1 (bases 1 to 405)  
Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,  
Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,  
Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.,  
and Shinzaki, K.  
Large scale analysis of Arabidopsis full-length cDNA (2002b)  
Unpublished (2002)  
Contact: Motoaki Seki  
Plant Functional Genomics Research Group  
RIKEN Genomic Sciences Center

TITLE  
JOURNAL  
COMMENT  
Email: meki@rcc.riken.go.jp  
An Arabidopsis full-length cDNA library was constructed essentially  
as reported previously (Seki et al., 1998). cDNA cleaved with BamHI  
and XhoI was ligated to modified lambda PhiC-1 vector (Carninci et  
al., submitted for publication) digested with BamHI and SalI. This  
clone is in a modified pluscript vector. Please visit our web

3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
Tel: 81-298-36-4359  
Fax: 81-298-36-9060  
Email: msekic@rken.go.jp

An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI and XhoI was ligated to modified Lambda F1C-1 vector (Carninci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pBluescript vector. Please visit our web site ([http://www.gsc.riken.go.jp/e/plant/index\\_e.html](http://www.gsc.riken.go.jp/e/plant/index_e.html)) for further details.

## FEATURES

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BASE COUNT  
ORIGIN

Query Match 22.9%; Score 386.6; DB 10; Length 405;  
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Matches 400; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
  
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Qy 1267 TATTCCTTTCTTCAACGCGATCTTAGGTCTTATCGAGCAGCTTCTCTGGCCTTTAA 1326  
Db 345 TATTCCTTTCTTCAACGCGATCTTAGGTCTTATCGAGCAGCTTCTCTGGCCTTTAA 286  
  
Qy 1327 CGGTATTATTCCTGTGGAGATGCACATTCACCAAGATTAAAGATCTCTGCTA 1386  
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Qy 1387 GATGGATTGCGCTGAAACGATGTGCTATGTTTGGCTGA-TCGCTCGCTCTTAGCTGCA 1445  
Db 225 GATGGATTGCGCTGAAACGATGTGCTATGTTTGGCTGCTCGCTCTTAGCTGCA 166  
  
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Db 165 GCCGGATCCATCCGAGACTTATAGTGTCTCAAACTCAAGCCCTCCGGACTATG 106  
  
Qy 1506 CATGAGTGAGTTGAGATCTCAAGAGAGTCAAAATATATGTAGTAGTTTGGTCTTCT 1565  
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Search completed: December 1, 2002, 10:30:59  
Job time : 2062 secs